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Result
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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1: /cgn2_6/ptodata/1,
2: /cgn2_6/ptodata/1,
3: /cgn2_6/ptodata/1,
4: /cgn2_6/ptodata/1,
5: /cgn2_6/ptodata/1,
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Copyright (c) 1993 - 2000 Com
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/cgn2_6/ptodata/1/ina/6B_COMB.seq:*
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US-08-192-480A-1
US-08-192-480A-1
US-08-194-574-6
US-08-911-423-5
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US-08-959-941-1
US-08-259-941-1
US-08-259-941-1
US-09-286-529-19
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US-08-765-907A-7
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Sequence 1, Appli Sequence 1, Appli	20,			Sequence 14, Appl	Sequence 4, Appli	Sequence 4, Appli	•	Sequence 22, Appl	Sequence 22, Appl	•	Sequence 23, Appl	Sequence 23, Appl	Sequence 23, Appl	Sequence 1, Appli

ALIGNMENTS

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RESULT 1
US-08-147-784-1
; NAME/KEY: CDS; LOCATION: 15..845; OTHER INFORMATION: US-08-147-784-1
                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/147,784
FILING DATE: 03-NOV-1993
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Smith, Willaim M
REGISTRATION NUMBER: 05490A-220
REFERENCE/DOCKET NUMBER: 05490A-220
TELECPHONE: (415) 326-2400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1, Application US/08147784 Patent No. 5821332
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APPLICANT: Godfrey, Wayne
APPLICANT: Buck, David
APPLICANT: Engleman, Edgar G.
TITLE: OF INVENTION: RECEPTOR ON THE SURFACE OF ACTIVATED
TITLE OF INVENTION: CD4+ T-CELLS: ACT-4
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                       TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1057 base pairs
TYPE: nucleic acid
GTEANTENEECE. 5:501
                                                                                      FEATURE:
                                                                                                          MOLECULE TYPE: HYPOTHETICAL:
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STATE: California
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Best Local Matches 10:

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0; Mismatches
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APPLICANT:
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COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
COMPUTER: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/195,967
FILING DATE: 10-FEB-194
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 05490A-230
TELECOMMUNICATION INFORMATION:
TELEPAN: (415) 326-2420
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LEEGTH: 1057 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                     INAME/KEY: CDS
LOCATION: 15.845
OTHER INFORMATION:
US-08-195-967-1
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Best Local Similarity 99.0
Matches 1056; Conservative
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STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94301
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APPLICANT: Engleman, Edgar G.
TITLE OF INVENTION: LIGAND (ACT-4-L) TO A RECEPTOR ON THE SURFACE OF ACTIVATED
TITLE OF INVENTION: CD4+ T-CELLS
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
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MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS: single
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tcagctccaagccgtgcaagcccttgcacgtggtgtaacctcagaagtggggagtgagcgga
                                                    ACCCCAGCAACGACCGGTGCTGCCACGAGTGCAGGCCAGGCAACGGGATGGTGAGCCGCT
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Pred. No. 3.2e-189;
0; Mismatches 1;
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RESULT 3
US-08-472-940-1
                                                                                                                                         Sequence 1, Application US/08472940 Patent No. 6277962 GENERAL INFORMATION:
                                                   GENERAL INFORMATION:
APPLICANT: Godfrey, Wayne
APPLICANT: Buck, David
APPLICANT: Engleman, Edgar G.
TITLE OF INVENTION: RECEPTOR ON THE S
TITLE OF INVENTION: CD4+ T-CELLS: ACT
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Kh
                                                                                                                                                                                                                                           1021
STREET: 379 Lytton
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94301
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                                f: 379 Lytton Avenue Palo Alto
                                                                                     ON THE SURFACE ELLS: ACT-4
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; FEATURE:
; NAME/KRY: CDS
; LOCATION: 15..845
; OTHER INFORMATION:
US-08-472-940-1
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Best Local Similarity
Matches 1056; Conserv
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MEDIUM TYPE: FIOPPY
MEDIUM TYPE: FIOPPY
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
OPTWARE: Patentin Release #1.0, Ver
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/472,940
FTI,ING DATE: 06-UN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 05
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US OF FILING DATE: 03-NOV-1993 ATTORNEY/AGENT INFORMATION: NAME: Smith, Willaim M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 06-JUN-
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
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Pred. No. 3.2e
0; Mismatches
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Gaps

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180

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540 480 480 420 420 360 360 300 300 240 240 180

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US-08-192-480A-1
                                                        ADDRESSEE: Klarquist Sparkman Campbell
ADDRESSEE: Klarquist Sparkman Campbell
ADDRESSEE: Leigh & Whinston
STREET: 121 S.W. Salmon Street, Suite 160
STATE: Oregon
COUNTRY: United States of America
21P: 97204
COMPUTER READBLE FORM:
MEDIUM TYPE: Disk, 3-1/2 inch
COMPUTER: IBM PC compatible
OPERATING SYSTEM: MS DOS
SOFTWARE: WOOGDERIC 5.1
CURRENT APPLICATION DATA:
APPLICATION UMBER: US/08/192,480A
FILING DATE:
CLASSIFICATION UMBER: US/08/192,480A
FILING DATE:
FILING DATE:
FILING DATE:
THEODMATTON.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1, Application US/08192480A Patent No. 5759546 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: TREATMENT OF CD4 T-CELL TITLE OF INVENTION: MEDIATED CONDITIONS NUMBER OF SEQUENCE: 3 CORRESPONDENCE ADDRESS:
ATTORNEY/AGENT INFORMATION:
NAME: Richard J. Polley,
REGISTRATION NUMBER: 28,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Andrew D. 1
APPLICANT: Vandenbark
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         28,107
 4282-38649
                                                                                                                                                                                                                                                                                                                         Suite 1600
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; MOLECULE TYPE: CDN
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRACMENT TYPE:
US-08-192-480A-1
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Best Local :
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TELEPHONE: (503) 226-7391
TELEPAX: (503) 228-9446
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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TYPE: Nucleic acid
STRANDEDNESS: Double
TOPOLOGY: Linear
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 CCCTGTACCTGATCCGGAGGGACCAGAGGCTGCCCCCGATGCCCACAAGCCCCCTGGGG
           ccctgtacctgctccggagggaccagaggctgccccccgatgcccccaaagccccctgggg
                                                     CCGCCATCCTGGGACTGGGGACTGGTGCTGGGGCCTGCTGGACATCCTGCTGG
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No. 7.9e-146;
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LOCATION: 1..1317;
SEQUENCE DESCRIPTION: SEQ
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US-08-097-827-10
S-08-097-827-10
; Sequence 10, Application US/08097827
; GENERAL INFORMATION:
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FILING DATE: 23-Jul-193
CLASSIFICATION: <UNKnown>
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patticia A.
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2806
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-587-0730
INFORMATION FOR SEQ ID NO: 10:
                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                      Matches
                                                                                      147
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STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: OPERATING SYSTEM: PC-DOS/MS-DOS
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IMMEDIATE SOURCE:
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                                                                      gagtgcaggccaggcaacgggatggtgagccgctgcagccgctcccagaacacggtgtgc 206
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Fanslow, William
Gayle, Richard
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66.6%;
                                                                                                                                                                                   Score 286.6; 1
Pred. No. 3e-4
0; Mismatches
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                                                                        FILING DATE: 22-JUN-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/0
FILING DATE: 23-JUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: PERKINS, PATTICLA A.
REGISTRATION NUMBER: 124 CO.
     INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Baum, Peter
APPLICANT: Goodwin, Ray
APPLICANT: Fanslow, William
APPLICANT: Gayle, Richard
TITLE OF INVENTION: No. 5783665el Cytokine Which is a Ligand
TITLE OF INVENTION: 0040
                             REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 28
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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TITLE OF INVENTION:

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US-08-494-574-10
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                                                 Sequence 6, Application US/08097827 GENERAL INFORMATION:
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Best Local Similarity 66.6%;
Matches 428; Conservative
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LENGTH: 1317 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IMMEDIATE SOURCE:
CLONE: MOX40Fc Mutein
FEATURE:
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                                        APPLICANT:
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           Goodwin, Ray
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Gayle, Richard
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Pred. No. 3e-46;
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Best Local Similarity 70.0
Matches 394; Conservative
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WEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Vei
CURRENT APPLICATION NUMBER: US/08/097,827
FILING DATE: 23-Jul-1993
CLASSIFICATION: (Unknown)
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia A.
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2806
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                      267
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
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                                          GTTGACTGTTCCCTGCCCTCCTGGCCACTTTTCTCCAGGCAACAACCAGGCCTGCAAG
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                                                                                                 ACTGTCTGCAGATGTAGACCAGGCACCCAACCTCGGCAGGACAGCGGCTACAAGCTTGGA
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LOCATION:
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STRANDEDNESS: single
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Pred. No. 1.3e-45;
0; Mismatches 158;
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US-08-494-574-6
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US-08-494-574-6
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                Best Local Sim
Matches 394;
                              Query Match
Best Local Similarity
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                                                                                                                                                                         MOLECULE TYPE: CDN
HYPOTHETICAL: NO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
CPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
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APPLICANT:
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APPLICANT: Gayle, Richard
TITLE OF INVENTION: NO. 5783665el Cytokine Which is
TITLE OF INVENTION: OX40
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 618 base pairs
                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/O
FILING DATE: 23-JUL-1993
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                    FEATURE:
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CITY: Seattle
STATE: WA
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                                                                                                                                                                                                                                                                                                                                         NAME: Perkins, Patricia A. REGISTRATION NUMBER: 34,693 REFERENCE/DOCKET NUMBER: 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08/494,574 FILING DATE: 22-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
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                                                                                                                                                                                                                                                                  618 base pairs
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Fanslow, William
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               Score 283.2; DB 1
Pred. No. 1.3e-45;
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US-08-911-423-3
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                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/023,419
FILING DATE: .16-AUG-1996
                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Gorman, Daniel M. APPLICANT: Randall, Troy D. APPLICANT: Zlotnik, Albert
               PRIOR APPLICATION DATA:
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                                                                                                                                                                                                         COUNTRY:
ZIP: 943
                                                                      APPLICATION NUMBER: US/08/911,423 FILING DATE: 14-AUG-1997 CLASSIFICATION: 536
                                                                                                                                                                                                                                   STREET: 901 California Avenue
CITY: Palo Alto
STATE: California
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APPLICATION NUMBER:
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                                                                                                                                                                                                        TRY: USA
94304-1104
                                                                                                                                                                                                                                                                                DNAX Research Institute
                                                                                                                                                                                                                                                                                                                                         MAMMALIAN CELL SURFACE ANTIGENS; RELATED
                                                                                                                                                                                                                                                                                                                           REAGENTS
 US 60/027,901
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US-08-911-423-3
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Best Local Similarity
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TELEFAX: 650-496-1200
INFORMATION FOR SEQ ID NO: 3:
      FILING DATA:
CLASSIFICATION: 536
CREATER APPLICATION DATA:
APPLICATION NUMBER: US 60
APPLICATION NUMBER: 16-AUG-1996
                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                       SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/911,423 FILING DATE: 14-AUG-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION: TELEPHONE: 650-852-9196
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                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION:
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LOCATION: 1..723
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                                                                                                                                                                                                                 COUNTRY:
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APPLICATION DATA:
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Zlotnik, Albert
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                             US 60/023,419
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; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
US-08-911-423-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
INFORMATION FOR SEQ ID NO:
                                                                                APPLICATION NUMBER: US/07/
FILING DATE: 19920911
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Ribando, Curtis P
                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Cheung, Av APPLICANT: Wesley, R APPLICANT: Wesley, R TITLE OF INVENTION: TITLE OF INVENTION: NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: DX
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-852-9196
                                                                                                                                                                              COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                      COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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LENGTH: 723 base pairs
TYPE: nucleic acid
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                            TELECOMMUNICATION INFORMATION:
TELEPHONE: 309-685-4011 ext.513
                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                   STREET: Peoria
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                                                                        REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                              ZIP:
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Ronald D.
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5352596th University Street
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SEQUENCE CHARACTERISTICS: LENGTH: 8438 base pair

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RESULT 12
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; LOCATION:
US-07-945-283-1
                                                      Sequence 1, Application US/07959941 Patent No. 5364781 GENERAL INFORMATION:
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Best Local Similarity
Matches 181; Conserv
                           APPLICANT:
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    APPLICANT:
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NAME/KEY:
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TYPE: NUCLEIC ACID
STRANDEDNESS: double
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HUTCHINSON, Charles R.
MADDURI, Krishna M.
TORTI, Francesca
COLOMBO, Anna L.
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; LOCATION:
US-07-959-941-1
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Best Local Similarity
Matches 187; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 16
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LENGTH: 1632 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE:
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PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: FILING DATE: 199210
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20005-5701
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ilarity 48.8%;
Conservative
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US-08-259-924-1
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Best Local
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COUNTRY: U.S.A.
COUNTRY: U.S.A.
ZIP: 20005-5701
COMPUTER REALABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPALIBLE
CONTROL TYPE: TOPOS/MS-DOS
COLOR TYPE: TOPOS/MS-DOS
                                                                                                                                                                                                                                                                                                Matches
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INFORMATION FOR SEQ ID NO: 1:
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APPLICATION NUMBER: US 07/959,941
FILING DATE: 09-OCT-1992
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APPLICANT: COLOMBO, Anna L.
TITLE OF INVENTION: PROCESS FOR PREPARING DAUNORUBICIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: HUTCHINSON, Charles
APPLICANT: MADDURI, Krishna M.
APPLICANT: TORTI, Francesca
APPLICANT: COLOMBO, Anna L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE:
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REGISTRATION NUMBER: 36,105
REFERENCE/DOCKET NUMBER: 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS:
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TGCGACTGATCCGCCACCTGGTGGCGATCGGACTGCTCGAGGAGGACGCACCGGGCGAGT
                          cctggccaagatctgaccttgggcccaccaaggtggacgctg-ggccccgccaggctgga 891
                                                                                                      ctgggggaggcagtttccggaccc--ccatccaagaggagcaggccgacgcccactccac
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DEDNESS: double
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1632 base pairs
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Pred. No. 0.29;
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Best Local :
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APPLICANT: Truneh, Alem
APPLICANT: Young, Peter
TITLE OF INVENTION: Tumoo
TITLE OF INVENTION: TR4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/794,796
                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: GH
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5219
                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 514
PRIOR APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline
STREET: 709 Swedeland
                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION: NAME: Han, William T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
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CITY: King of Prussia
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TOPOLOGY: 11
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ggctgagcaccgtgacggggctccactgtgtcgggggacaccttaccccagcaacggcaacggt 138
                                         GGCACGACCTGACGCAGGCCGTGGCGCGCCGACATCTCCTTCACCCGCCTCCCCGACG 579
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; TYPE: DNA
; ORGANISM: Homo sapien
US-09-286-529-18
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Patent No. 6297367
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Catherine Tribouley
TITLE OF INVENTION: NEW MEMBERS OF THE AND THE FAMILIES
FILE REFERENCE: 1408.003/200130.439C1
CURRENT APPLICATION NUMBER: US/09/286,529
CURRENT FILING DATE: 1999-04-05
NUMBER OF SEQ ID NOS: 25
NUMBER OF SEQ ID NOS: 25
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: 1
SEQ ID NO 18
                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 4.5%;
Best Local Similarity 46.4%;
Matches 154; Conservative
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460 tgtgcgcccagtgcccccaggcacctttgtgcagcggccgtgccgccgagacagcccca 519
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Search completed: June 18, 2002, 17:24:04 Job time: 10162 sec

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Post-processing: Minimum Match 0%
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Listing first 45 summaries
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Copyright (c) 1993 - 2000 Compugen Ltd.
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alpha-1 ch
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C:Species: Homo sapiens (man)
C:Species: Homo sapiens
C:Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 11-Jan-2000
C:Accession: I37552
R:Latza, U: Durkop, H: Schnittger, S: Ringeling, J: Eitelbach, F: Hummel, Eur. J. Immunol. 24, 677-683, 1994
A;Title: The human OX40 homolog: cDNA structure, expression and chromosomal ass Reference number: I37552; MUID:94170844
A;Accession: I37552
A;Status: preliminary: translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-277 CRES-
A;Cross-references: EMBL:X75962; NID:9472957; PIDN:CAA53576.1; PID:9472958
C;Superfamily: CD27 antigen: NGF receptor repeat homology
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122 122	122.5	125 124.5	125.5	126 126	126.5	127	127.5	128	128.5	132	138
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T23433 T37316	T26972 I48161	T28811 GQHUT1	I48324	A55677	S53868	T15099	S18252	T10053	A55347	MMRTS	S53869
hypothetical prote probable laminin a	hypothetical prote p-185 precursor -	hypothetical prote tumor necrosis fac	DELTA-like 1 - mou	laminin beta-2 cha	laminin alpha-2 ch	hypothetical prote	heparan sulfate pr	laminin alpha 5 ch	adhesive ligand ep	laminin beta-2 cha	laminin beta-2 cha

ALIGNMENTS

chromosomal assignmen

: : Fo

RESULT 2 S12783 S12783 S12783 S12783 N;Alternate names: nerve growth factor receptor homolog C;Species: Rattus norvegicus (Norway rat) C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 05-Nov-1999 C;Accession: S12783; S08036 R;Mallett, S; Fossum, S; Barclay, A.N. EMBO J. 9, 1063-1068, 1990	Qy 241 RRDQRLPPDAHKPPGGGSFRTPIQEEQADAHSTLAKI 277	Qy 181 GPPARPITVQPTEAWPRTSQGPSTRPVEVPGGRAVAAILGLGLVLGLLGPLAILLALYLL 240 	Qy 121 PGVDCAPCPPGHFSPGDNQACKPWTNCTLAGKHTLQPASNSSDAICEDRDPPATQPQETQ 180	Qy 61 NTVCRPCGDGFYNDVVSSKPCKPCTWCNLRSGSERKQLCTATQDTVCRCRAGTQPLDSYK 120	Qy 1 MCVGARRLGRGPCAALLLLGLGLSTVTGLHCVGDTYPSNDRCCHECRPGNGMVSRCSRSQ 60	Query Match 100.0%; Score 1538; DB 2; Length 277; Best Local Similarity 100.0%; Pred. No. 5e-94; Matches 277; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
gene ox40 protein - mouse

N;Alternate names: OX40 antigen

C;Species: Mus musculus (house mouse)

C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 11-Jan-2000

C;Accession: I48700; I48334; S34377

R;Calderhead, D.M.; Buhlmann, J.E.; van den Eertwegh, A.J.; Claassen, E.; Noelle
J. Immunol. 151, 5261-5271, 1993

A;Reference number: I48700; MUID:94044750

A;Accession: I48700
A;Accession: I48704
A;Residues: 1-272 <RES>
A;Cross-references: EMBL:221674; NID:g312827; PIDN:CAA79772.1; PID:g312828
R;Birkeland, M.L.; Copeland, N.G.; Gilbert, D.J.; Jenkins, N.A.; Barclay, A.N.
Eur. J. Immunol. 25, 926-930, 1995
Eur. J. Immunol. 25, 926-930, 1995
Eur. J. Immunol. 25, 926-930, 1995
A;Reference number: I48334; MUID:95255413
A;Accession: I48334
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-14,'G',16-272 <RE2>
A;Conse: ox40
A;Introns: 45/1; 86/1; 122/1; 144/2; 210/1; 250/1
C;Superfamily: CD27 antigen; NGF receptor repeat homology
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A;Accession: $12783
A;Accession: $12783
A;Molecule type: mRNA
A;Residues: 1-271 cMAL>
A;Cross-references: EMBL:X17037; NID:g57830; PIDN:CAA34897.1; PC;Superfamily: CD27 antigen; NGF receptor repeat homology C;Superfamily: CD27 antigen; NGF receptor transmembrane protein F;1-19/Domain: signal sequence #status predicted cMAT>
F;21-235/Domain: transmembrane #status predicted cTMM>
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Best Local S
Matches 168
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EAWPRTSQGPSTRPVEVPGGRAVAAILGLGLVLGLLGPLAILLALYLLRRDQRLPPDAHK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FSPGDNQACKPWTNCTLAGKHTLQPASNSSDAICEDRDPPATQPQETQGPPARPITVQPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VVSSKPCKPCTWCNLRSGSERKQLCTATQDTVCRCRAGTQPL--DSYKPGVDCAPCPPGH 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AFLLLGLSLGVTVKLNCVKDTYPSGHKCCRECQPGHGMVSRCDHTRDTVCHPCEPGFYNE
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                  55.7%;
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Pred.
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Pred. No. 6.
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    Mismatches
                  857; DB 2;
No. 2.1e-49;
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                                     Length 272;
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6,
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A;Cross-references: GB:M14764; NID:g189204; PIDN:AAB59544.1; PID:g189205
R;Marano, N.; Dietzschold, B.; Earley Jr., J.J.; Schatteman, G.; Thompson, S.;
J. Neurochem. 48, 225-232, 1987
A;Title: Purification and amino terminal sequencing of human melanoma nerve gro
A;Reference number: A60204; MUID:87085574
A;Rocession: A60204
A;Rocession: A60204
A;Rocession: A60204
A;Rosidues: 29-31, 'T', 33-42, 'TT', 45-46, 'TX', 50-51, 'XX', 54-56 <MAR>
A;Rosidues: 29-31, 'T', 33-42, 'TT', 45-46, 'TX', 50-51, 'XX', 54-56 <MAR>
A;Rosidues: 29-31, 'T', 33-42, 'TT', 45-46, 'TX', 50-51, 'XX', 54-56 <MAR>
A;Rote: this sequence has been corrected by a note added in proof to follow the
R;Vissavajjhala, P.; Leszyk, J.D.; Lin-Goerke, J.; Ross, A.H.
R;Vissavajjhala, P.; Leszyk, J.D.; Lin-Goerke, J.; Ross, A.H.
A;Title: Structural domains of the extracellular domain of human nerve growth i
A;Reference number: S21689; MUID:92198017
A;Scatus: prelininary
A;Malcoule type: Toretan
C;Comment: T
C;Comment: T
C;Comment: T
C;Genetics:
                  A;Cross-references: GB:M21621; NID:g189206; PIDN:AAA36363.1; PID:g189207 C;Comment: This receptor is found on sensory and sympathetic neurons, on C;Comment: The cysteine-rich region of the extracellular domain may form C;Comment: This protein is thought to form a high-affinity receptor when C;Comment: This receptor undergoes both N- and O-linked glycosylation.
                                                                                                                                                                                                                            A; Molecule type: protein
A; Residues: 183-208 <VIS>
R; Sehgal, A; Patil, N; Chao, M.
R; Sehgal, A; Patil, N; Chao, M.
Mol. Cell. Biol. 8, 3160-3167, 1988
Mol. Cell. Biol. 8, 3160-3167, Mol. Reference number: 157638, MOUTD: 89096903
A; Accession: 157638
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C:Date: 31-Mar-1988 #sequence_revision 31-Mar-1988 #text_change C:Accession: A25218; A60204; S21689; 157638 R:Johnson, D:, Lanahan, A.; Buck, C.R.; Sehgal, A.; Morgan, C.; Cell 47, 545-554, 1986
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A; Residues: 1-22 <RES>
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A; Residues: 1-427 <JOH>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C; Species: Homo sapiens (man)
C; Date: 31-Mar-1988 #sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      and structure of the human A25218; MUID:87051725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      receptor precursor,
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A; Map position: 17q21-17q22 C; Superfamily: nerve growth factor receptor; C; Keywords: duplication; glycoprotein; hetero E;1-28/Domain: signal sequence #status predic

eptor; NGF receptor repeat homology

phosphoprotein;

receptor

er; monomer; <SIG>

predicted

A; Cross-references:

GDB:120234;

OMIM: 162010

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A:Map position: 20q12-20q13.2
C:Superfamily: CD27 antigen; NGF receptor repeat homology
C:Keywords: B-cell; glycoprotein; phosphoprotein; surface antigen; transmembrane
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-277/Product: B-cell activation protein CD40 #status experimental <MAT>
F:21-193/Domain: extracellular #status predicted <EXT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A60771
B-cell activation protein CD40 precursor - human
N;Alternate names: B-cell surface antigen Bp50
C;Species: Homo sapiens (man)
C;Date: 03-Jun-1993 #sequence_revision 03-Feb-1994 #text_change
C;Accession: S04460; A60771
C;Accession: S04460; A60771
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                                                                                                                                                                                                                                                                                                           A; Accession: A60771
A; Molecule type: protein
A; Residues: 21-50 <BRA>
                                                                                                                                                                                                                                                                                                                                                                                A; Title: Biochemical characteristics and partial amino A; Reference number: A60771; MUID:89093941
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Title: A B-lymphocyte activation molecule related A;Reference number: S04460; MUID:89356608 A;Accession: S04460
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F; 153, 180/Binding
                                                                                                                                                                                                            A;Cross-references: GDB:215268; OMIM:109535
                                                                                                                                                                                                                                     A; Gene: GDB:CD40
                                                                                                                                                                                                                                                                C; Genetics:
                                                                                                                                                                                                                                                                                       A; Experimental source:
                                                                                                                                                                                                                                                                                                                                                                                                                                J. Immunol. 142, 562-567, 1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: EMBL:X60592; NID:g29850; PIDN:CAA43045.1;
R;Braesch-Andersen, S.; Paulie, S.; Koho, H.; Nika, H.; Aspen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: mRNA
A; Residues: 1-277 <STA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBO J. 8, 1403-1410, 1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R;Stamenkovic,
                      ;194-215/Domain:
;216-277/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               251-272/Domain:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           194
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 VGARRIGR---GP-CAALLLIGIGI----STVTGLHCVGDTYPSNDRCCHECRPGNGMV 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MGAGATGRAMDGPRLLLLLLLGVSLGGAKEACPTGL-----YTHSGECCKACNLGEGVA 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AGVVTTVMGSSQPVVTRGTTDNLIPVYCSILAAVVVGLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AWPRTSQGPSTRPVE-----VPGGRAVAAILGLGLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     E-DTERQLRECTRWADAECEEIPGRWITRSTPPEGSDSTAPSTQEPEAPPEQDL-IASTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TLAGKHTLQPASNSSDAICED------RDPPATQPQETQGPPARPITVQPTE 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    YGYYQDETTGRCEACRVCEAGSGLVFSCQDKQNTVCEECPDGTYSDEANHVDPCLPCTVC 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QPCGANQ-TYCEPCLDSYTFSDYVSATEPCKPCTECYGLQSMSAP---CYEADDAYCRCA 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SRCSRSQNTVCRPCGPGF-YNDVVS-SKPCKPCTWC-NLRSGSERKQLCTATQDTVCR-- 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                84;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     site:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              I.; Clark,
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intracellular #status predicted <INT>
carbohydrate (Asn) (covalent) #status
                        transmembrane #status predicted <TMM> intracellular #status predicted <CYT>
  site: carbohydrate (Asn)
                                                                                                                                                                                                                                                                                    Burkitt lymphoma
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -CRAGTQPLDSY--KPGVDCAPCPPGHFSPGDNQA--CKPWTNC 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           31;
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Pred.
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  (covalent) #status
                                                                                                                                                                                                                                                                                       Raji
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stroem, P.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  growth factor receptor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Perlmann,
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Best Local S
Matches 66
                                                                187
                                                                                              175
                                                                                                                              135
210
                              235 LALYLLRRDQRLP----PDAHKPP-----GGGSFRTPIQE 265
                                                                                                                                                              125
                                                                                                                                                                                            75
                                                                                                                                                                                                                              80
                                                                                                                                                                                                                                                            15
                                                                                                                                                                                                                                                                                           26
                                                                                                                                                                                          THCHQHKYCDPNLGLRVQQKGTSETDTICTCEEGWHCTSEACESCVLHRSCSPGFGVKQI 134
                                                                                                                                                                                                                           P-CKPCTWCNLRSGSERKQLCTATQDTVCRCRAGTQPLD-----
                                                                                                                                                                                                                                                           LTAVHPEPPTACREKQYLINSQCCSLCQPGQKLVSDCTEFTETECLPCGESEFLDTWNRE 74
                                                                                                                                                                                                                                                                                           VTGLH-----CVGDTYPSNDRCCHECRPGNGMVSRCSRSQNTVCRPCGPGFYNDVVSSK 79
LVLVFIKKVAKKPTNKAPHPKQEPQEINFPDDLPGSNTAAPVQE 253
                                                                                              QPQETQGPPARPITVQPTEAWPRTSQGPSTRPVEVPGGRAVAAILGLGLVLGLLGPLAIL
                                                                                                                            ATGVSDTICEPCPVGFFSNVSSAFEKCHPWTSCETKDLVVQQAGTNKTDVVC-----
                                                                                                                                                                                                                                                                                                                           l Similarity
66; Conserv
                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                       -CAPCPPGHFSPGDN--QACKPWTNCTLAGKHTLQPASNSSDAICEDRDPPAT 174
                                                                                                                                                                                                                                                                                                                       14.4%; Score 221.5; DB 2
23.2%; Pred. No. 9.1e-08;
Live 34; Mismatches 95
                                                            -----GPQDR-----LRALVVIPIIFGIL--FAIL 209
                                                                                                                                                                                                                                                                                                                                                       DB 2;
                                                                                                                                                                                                                                                                                                                                                     Length
                                                                                                                                                                                                                           ----SYKPGVD----
                                                                                                                                                                                                                                                                                                                                                           277;
                                                                                                                                                                                                                                                                                                                           89;
                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                              234
                                                                                                                              186
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A; Decles: Free: mRNA
A; Molecule type: mRNA
A; Rolecule type: mRNA
A; Residues: 1-195 'R', 197-461 < KOH>
A; Residues: 1-195 'R', 197-461 < KOH>
A; Residues: 1-195 'R', 197-461 < KOH>
A; Cross references: GB.M55994; GB.M38549; NID:g339757; PIDN:AAA36755.1; PID:g339758
A; Cross references: GB.M55994; GB.M38549; NID:g339757; PIDN:AAA36755.1; PID:g339758; PID:g339 R;Smith, C.A.; Davis, T.; Angerson, D., Comm., T., T., Science 248, 1019-1023, 1990
Science 248, 1019-1023, 1990
A;Title: A receptor for tumor necrosis factor defines an unusual family of cellular A;Reference number: A35356; MUID:90260639 A;Title: A second tumor necrosis factor receptor gene A;Reference number: A36475; MUID:91045991 A;Accession: A36475 C;Species: Homo sapiens (man)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 08-Dec-2000 C;Accession: A35356; A36475; A48416; A36007; A23666; B35010; I38094 C;Accession: A35356; A36475; A48416; A36007; A23666; B35010; I38094 A;Cross-references: GB:M32315; NID:g189185; PIDN:AAA59929.1; PID:g189186 R;Kohno, T.; Brewer, M.T.; Baker, S.L.; Schwartz, P.E.; King, M.W.; Hale Proc. Natl. Acad. Sci. U.S.A. 87, 8331-8335, 1990 A;Status: A; Molecule type: mRNA A; Residues: 1-461 <SMI> A;Status: tumor necrosis factor receptor 2 precursor (validated) N;Alternate names: 75K tumor necrosis factor receptor; TI preliminary preliminary product TNF receptor type can shed a Hale, naturally oc K.K.; Squir

Brockhaus,

A;Residues: 23-461 (DEM>
A;Cross-references: GB:S63368; NID:9235648; PIDN:AAB19824.1; PID:9235649
A;Cross-references: GB:S63368; NID:9235648; PIDN:AAB19824.1; PID:9235649
A;Note: sequence extracted from NCBI backbone (NCBIN:63368, NCBIP:63371)
R;Heller, R.A.; Song, K.; Onasch, M.A.; Fischer, W.H.; Chang, D.; Ringold Proc. Natl. Acad. Sci. U.S.A. 87, 6151-6155, 1990
A;Title: Complementary DNA cloning of a receptor for tumor necrosis facto A;Reference number: A36007; MUID:90349572
A;Reference : A36007 R; Dembic, Z.; Loetscher, H.; Gubler, U.; Pan, Cytokine 2, 231-237, 1990
A;Title: Two human TNF receptors have similar A; Reference number: A48416; MUID:91370690
A; Accession: A48416 A;Status: preliminary extracellular, but distinct D.; Ringold, intracellul ന ഷ

for tumor necrosis factor and

A;Molecule type: mRNA A;Residues: 116-140,'P',142-195,'R',197-362,'T',364-461 <HEL> A;Residues: 116-140,'P',142-195,'R',197-362,'T',364-461 <HEL> A;Cross-references: GB:M35857; NID:g339751; PIDN:AAA63262.1; PID:g339752 R;Loetscher, H.; Schlaeger, E.J.; Lahm, H.W.; Pan, Y.C.E.; Lesslauer, W.; J. Biol. Chem. 265, 20131-20138, 1990 A; Status: preliminary Purification and partial amino acid sequence analysis of. two distinct Brockhaus,

tumor

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X; Enjethenn, H.; NOVICK, D.; Wallach, D.

X; Elol. Chem. 265, 131-1536, 1990

A; Title: Two tumor necrosis factor-binding proteins purified from human urine.
A; Reference number: A35010; MUID:90110215

A; Accession: B35010

A; Status: preliminary
A; Molecule type: protein
A; Residues: 27-31 < ENKO
A; Richart, P.; Kemper, O.; Wallach, D.
Gene 150, 381-386, 1994

A; Title: Cloning, sequencing and partial functional characterization of the 5'
A; Reference number: I38094; MUID:95121934

A; Recession: I38094; MUID:95121934

A; Recession: I38094; MUID:95121934

A; Recession: I38094; MUID:95121934

A; Recession: I38094; MUID:95121934

A; Retarence number: I38094; MUID:95121934

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A;Accession: A23666
A;Status: preliminary
A;Molecule type: protein
A;Residues: 23-40;65-69;1:
R;Engelmann, H.; Novick, I
                                                                                                                                RESULT
A26431
                   nerve growth factor receptor precursor, 1
N;Alternate names: NGF receptor
C;Species: Rattus norvegicus (Norway rat)
C;Date: 10-Sep-1999 #sequence_revision 10
C; Date: 10-Se
C; Accession:
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                                                                                                                                                                                                                                          EPSTAPSTSFLLPMGPSPPAEGSTGDFALPVGLIVGVTALGLLII
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                                                                                                                                                                                                                                                                                                                                                                                                      PWTNCTLAGKHTLQPASNSSDAICEDRDPPATQPQETQGPPA----RPITV--QPTEAWP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AKVFCTKTSDTVCDSCEDSTYTQLWNWVP--ECLSCGSRCSSDQVETQACTREQNRICTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MVSRCSRSQNTVCRPCGPGFYNDVVSSKPCKPCTWCNLRSGSER--KQLCTATQDTVCRC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PVAVWAALAVGLELWAAAHALPAQVAFTPYAPEPGSTCRLREYYDQTAQMCCSKCSPGQH
                                                                                                                                                                                                                                                                                                                                                    PHQICNVVA----IPGNASMDAVC----TSTSPTRSMAPGAVHLPQPVSTRSQHTQPTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                           RPGWYCALSKQEGCRLCAPLRKCRPGFGVARPGTETSDVVCKPCAPGTFSNTTSSTDICR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RAG------TQPLDSYKPG------VDCAPCPPGHFS--PGDNQACK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .; Novick, D.; Wallach, D. 265, 1531-1536, 1990 umor necrosis factor-binding mber: A35010; MUID:90110215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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                                                                                                                                                                                                                                                                                               -PVEVPGGRAVAAILGLGLVLGL--LGPLAI
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Pred.
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                      10-Sep-1999 #text_change 10-Sep-1999
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No. 2
                                                                                                         low
                                                                                                    affinity
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R; Large, T.H.; Weskamp, G.; Helder, weuron 2, 1123-1134, 1989
A; Title: Structure and developmental A; Reference number: JN0006; MUID:9016
A; Accession: JN0006

MUID: 90166579

of.

growth

factor

J.С.;

Radeke,

M.J.; Misko, f the nerve g

T.P.; Shooter,

E.M.; R

10-Sep-1999 #text_change 10-Sep-1999

C;Date: 10-Sep-1999 #sequence_revision C;Accession: JN0006; A60504

N; Alternate names: NGF receptor
C; Species: Gallus gallus (chicken)

nerve growth factor

receptor,

low affinity

precursor -

chicker

JN0006

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Gleenerand
A;Introns: 20/3
A;Introns: 20/3
C;Superfamily: nerve growth factor receptor; NGF receptor rej
C;Superfamily: nerve growth factor receptor; NGF receptor rej
C;Keywords: duplication; glycoprotein; heterodimer; monomer;
F;1-29/Domain: signal sequence #status predicted <SIG>
F;30-425/Product: nerve growth factor receptor #status predif
F;30-251/Domain: NGF receptor repeat homology <NG1>
F;33-65/Domain: NGF receptor repeat homology <NG2>
F;10-148/Domain: NGF receptor repeat homology <NG3>
F;110-148/Domain: NGF receptor repeat homology <NG3>
F;150-199/Domain: NGF receptor repeat homology <NG3>
F;150-199/Domain: NGF receptor repeat homology <NG4>
F;198-249/Region: serine/threonine-rich
F;252-273/Domain: transmembrane #status predicted <NEM>
F;274-4-25/Domain: intracellular #status predicted <INT>
Transmembrane #sta
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A;Cross-references: GB:X61269
C;Comment: This receptor is found on sensory and sympathetic neurons, on C;Comment: The cysteine-rich region of the extracellular domain may form C;Comment: This protein is thought to form a high-affinity receptor when C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: GB:X05137; NID:g56755; PIDN:CAA28783.1; PID:g56756 R;Mets1s, M.; Timmusk, T.; Allikmets, R.; Saarma, M.; Persson, H. Gene 121, 247-254, 1992 A;Title: Regulatory elements and transcriptional regulation by testost. A;Reference number: PH1229; MUID:93077038
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R; Radek
Nature
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A; Residues: 1-425 < RAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Accession: PH1229
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VADMVTTVMGSSQPVVTRGTTDNLIPVYCSILAAVVVGLV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RRLGRGPCAA-----LLLLGLGLST------VTGLHCVGDTYPSNDRCCHECRPGNGM 52
                                                            EAWPRTSQGPSTRPVE-----VPGGRAVAAILGLGLV
                                                                                                                                   CE-DTERQLRECTPWADAECEEIPGRWIPRSTPPEGSDSTAPSTQEPEVPPEQDL-VPST
                                                                                                                                                                                            CTLAGKHTLQPASNSSDAICED----
                                                                                                                                                                                                                                                                                                                                                                                                           AQPCGANQ-TVCEPCLDNVTFSDVVSATEPCKPCTECLGLQSMSAP---CVEADDAVCRC
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Pred.
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No. 3e-07;
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268
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C; Superfamily: tumor necrosis factor receptor type 1;

NGF receptor repeat homology

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R; Baens, M.; Chaffanet, M.; Cassiman, J.J. Genomics 16, 214-218, 1993
A; Title: Construction and evaluation of a A; Reference number: 154182; MUID:93252381
A; Accession: 154182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C:Comment: This receptor is found on sensory and sympathetic neurons, on neuroblastoma of:Comment: The cysteine-rich region of the extracellular domain may form part or all of C:Comment: This protein is thought to form a high-affinity receptor when it associates of C:Superfamily: nerve growth factor receptor; NGF receptor repeat homology C:Keywords: duplication; glycoprotein; heterodimer; monomer; phosphoprotein; receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Species: Homo sapiens (man)
C;Date: 24-May-1996 #sequence_revision
C;Accession: I54182
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F;21-416/Product: nerve growth factor receptor *status predicted <MAT>
F;21-239/Domain: extracellular *status predicted <EXT>
F;24-57/Domain: NGF receptor repeat homology <NG1>
F;59-100/Domain: NGF receptor repeat homology <NG2>
F;50-100/Domain: NGF receptor repeat homology 
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    A;Cross-references:
A;Map position: 12pl
                                                                                                                                                                                                 A; Molecule type: mRNA
A; Residues: 1-435 < RES>
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F;262-416/Domain:
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A; Residues: 1-416 <LAR>
                                                                                    A; Gene: GDB: LTBR
                                                                                                                                                                   A; Cross-references:
                                                                                                                                                                                                                                                                                     A; Status: preliminary; translated
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12p13.3-12p13.1
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intracellular #status predicted <INT>
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                                          OMIM: 600979
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A;Note: sequence extracted from NCBI backbone (NCBIP:120357) C;Comment: For an alternative splice form, see PIR:A6675. C;Comment: For an alternative splice form, see PIR:A6476. C;Superfamily: CD27 antigen; NGF receptor repeat homology C;Keywords: alternative splicing; transmembrane protein F;105-144/Domain: NGF receptor repeat homology <NGF>
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A;Residues: 1-287,'LV' <GRI>
A;Cross-references: GB:M83312; NID:g1553058; PIDN:AAB08705.1; PID:g1553059;
A;Experimental source: BALB/c, liver
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A;Note: sequence extracted from NCBI backbone (NCBIN:75206, NCBIP:75207)
A;Note: this translation is not annotated in GenBank entry MUSCD40A, release R;Grimaldi, J.C.; Torres, R.; Kozak, C.A.; Chang, R.; Clark, E.A.; Howard,
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J. Immunol. 148, 620-626, 1992
A;TitLe: Differential increase of an alternatively polyadenylated
A:Terence number: A46476; MUID:92105763
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J. Immunol. 149, 3921-3926, 1992
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                                                                                                                                                                                                                                                                                                                                                                                                               A;Status: preliminary; not compared with conceptual translation
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                                                                                                                                       Query Match
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- PCKPCTWCNLRSGSERKQLCTATQDTVCRCRAG
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                                    LTAVHLGQCVTCSDKQYLHDGQCCDLCQPGSRLTSHCTALEKTQCHPCDSGEFSAQWNRE
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                                                                                                                Similarity 22.(
64; Conservative
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                                                                         -CVGDTYPSNDRCCHECRPGNGMVSRCSRSQNTVCRPCGPGFYNDVVSSK 79
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22.0%;
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No. 6.5e-07;
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oward, M.; Co
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B32393
T-cell antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Introns: 35/1; 69/1; 115/1; 138/2; 156/3; 181/1; 225/1 C;Superfamily: CD27 antigen; NGF receptor repeat homology C;Keywords: transmembrane protein F;1-23/Domain: signal sequence #status predicted <SIG>F;24-256/Product: 4-1BB protein #status predicted <MAT>
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A;Molecule type: DNA
A;Residues: 1-256 <RES>
A;Cross-references: EMBL:U02567; NID:g1117783; PIDN:AAA93113.1;
C;Genetics:
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A; Cross references: GB. J04492; NID: g201121; PIDN: AAA40167.1; A; Cross references: GB. J04492; NID: g201121; PIDN: AAA40167.1; A; Kwon, B.S.; Kozak, C.A.; Kim, K.K.; Pickard, R.T.  
J. Immunol. 152, 2256-2262, 1994
A; Title: Genomic Organization and Chromosomal Localization of A; Reference number: 148879; MUID: 94179805
A; Accession: 148879
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Reference number: A32393; MUID:89184547
A; Accession: B32393
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Proc. Natl. Acad. Sci. U.S.A. 86, 1963-1
A:Title: cDNA sequence of two inducible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Species: Mus musculus (house mouse)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 21-Jul-2000
C;Accession: B3239; 14887.
R;Kwon, B.S.; Welssman, S.M.
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A; Residues: 1-256 < KWO>
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                                                                                                                   GGGSFRTPIQEE
                                                                                                                                                              --PGGHSLQVLTLFLALTSALLLALIFITLLFSVLKWIRKKFPHIFKQPFKKTTGAAQEE
                                                                                                                                                                                                   EVPGGRAVAAI-LGLGLVLGLLGPLAILLALY-LLRRDQRLPPDAHKPP-----
                                                                                                                                                                                                                                              SLDGRSVLKTGTTEKDVVC---
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                                                                                                                       266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13.2%; Score 202.5; DB 2 25.4%; Pred. No. 1.5e-06;
                                                                                                                                                                                                                                                                                                                                                               -TQPLDSYKPGVD-----CAPCPPGHFSPGDNQ-ACKPWTNC
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C;Accession: I48854
R;Powell, E.B.; Wicker, L.S.; Peterson, L.B.; Todd, J.A.
Mamm. Genome 5, 726-727, 1994
A;Title: Allelic variation of the type 2 tumor necrosis
A;Reference number: I48854; MUID:95178848

factor

gene murine tumour necrosis factor receptor 2 protein - mouse (fragment)
C; Species: Mus musculus (house mouse)
C; Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 23-Jul-1

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A;Molecule type: DNA
A;Residues: 1-22 <KIS>
A;Residues: 1-22 <KIS>
A;Residues: 1-22 KIS>
A;Cross-references: EMBL:X87128; NID:g809043; PIDN:CAA60618.1; PID:g809044
A;Cross-references: EMBL:X87128; NID:g809043; PIDN:CAA60618.1; PID:g809044
C;Superfamily: tumor necrosis factor receptor type 2; NGF receptor repeat P;1-22/Domain: signal sequence #status predicted <SIG>F;23-474/Product: tumor necrosis factor receptor type 2 #status predicted <F;40-77/Domain: NGF receptor repeat homology <NG1>F;166-203/Domain: NGF receptor repeat homology <NG2>F;166-203/Domain: NGF receptor repeat homology <NG4>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Species: Mus musculus (house mouse)
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 23-Jul-1999
C;Accession: B38634; A40254; S54816
R;Lewis, M.; Tartaglia, L.A.; Lee, A.; Bennett, G.L.; Rice, G.C.; Wong, G.H.W.;
Proc. Natl. Acad. Sci. U.S.A. 88, 2830-2834, 1991
A;Title: Cloning and expression of cDNAs for two distinct murine tumor necrosis A;Reference number: A38634; MUID:91187885
A;Accession: B38634
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C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992
C;Accession: B38634; A40254: STARIF
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A;Residues: 1-474 <LEW>
A;Residues: 1-474 <LEW>
A;Cross-references: GB:M60469; NID:gl99827; PIDN:AAA39752.1; PID:gl99828
A;Cross-references: GB:M60469; NID:gl99827; PIDN:AAA39752.1; PID:gl99828
R;Goodwin, R.G.; Anderson, D.; Jerzy, R.; Davis, T.; Brannan, C.I.; Cope.
Mol. Cell. Biol. 11, 3020-3026, 1991
Mol. Cell. Biol. 11, 3020-3026, 1991
                                                                                                                                                                                                                                                                                            B
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A;Description: Characterization of the promoter region of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Title: Molecular cloning and expression A; Reference number: A40254; MUID: 91246168 A; Accession: A40254
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A; Residues: 1-474 <GOO>
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Best Local S
Matches 68
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13
                                                                               MLGLVNCIILVQRKKKPSCLQRDAKVPHVPD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CCAKCPPGQYVKHFCNKTSDTVCADCEASMYTQVWNQ--FRTCLSCSSSCTTDQVEIRAC 111
                                                                                                                                                                                                                                  PARPITVQPTEAWPRTSQGPS-----TRPV---EVPGGRAVAAILGLGLVLGLLGPLAI 233
                                                                                                                                                                                                                                                                                            SDTTSSTDVCRPHRICSILA----IPGNASTDAVCAPESPTLSAIPRTLYVSQPEPTRS-
                                                                                                                                                                                                                                                                                                                                          S--PGDNQACKPWTNCTLAGKHTLQPASNSSDAICEDRDP----PAT----QPQETQGP 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CCHECRPGNGMYSRCSRSQNTVCRPCGPGFYNDVVSSKPCKPCTWCNLRSGSERKQL--C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           68;
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                                                                                                                                                                                 QPLDQEPGPSQTPSILTSLGSTPIIEQSTKGG
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25.1%;
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Pred.
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No. 2.5e-06;
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                                                                                                                             249
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, Y.
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A; Molecule type: mRNA
A; Molecule type: mRNA
A; Residues: 1-106, 'R', 108-255 <SCH>
A; Residues: 1-106, 'R', 108-255 <SCH>
C; Comment: This protein belongs to a member of the human nerve-growth-factor/tumor-necrd C; Comment: This receptor recongnizes soluble, cell-surface bound or extracellular matrix C; Comment: This receptor; loss of the homology C; Keywords: glycoprotein; phosphoprotein; receptor; transmembrane protein F; 1-17/Domain: signal sequence #status predicted <SIG-
F; 18-255/Product: lymphocyte activation-induced receptor IIA #status predicted <MAT>
F; 138-255/Product: lymphocyte activation-induced receptor IIA #status predicted F; 138-149/Binding site: carbohydrate (Asn) (covalent) #status predicted F; 234, 235/Binding site: phosphate (Thr) (covalent) (by casein kinase C) #status predicted F; 242/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: EMBL:U03397; NID:g571320; R;Schwarz, H.; Tuckwell, J.; Lotz, M. Gene 134, 295-298, 1993 A;Title: A receptor induced by lymphocyte active A;Reference number: JT0752; MUID:94085794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         lymphocyte activation-induced receptor IIA precursor - human c;Species: Homo sapiens (man) C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_cha C;Accession: I38426; JT0752
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A; Accession: I38426
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Accession: I48854
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-459 <RES>
οy
                                                                                                                                                                                                                                                                                                                                                                                                            A; Accession: JT0752
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: mRNA
A; Residues: 1-255 < RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Status: preliminary; translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: EMBL:X76401; NID:g433830; PIDN:CAA53981.1; PID:g433831
C;Superfamily: tumor necrosis factor receptor type 2; NGF receptor repeat homology
F;151-188/Domain: NGF receptor repeat homology <NGF>
                                                                Query
Best I
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  262 LGLVNCFILVQRKKKPSCLQRDAKVPHVPD 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    101 ATQDTVCRCRAG---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   42 CCHECRPGNGMVSRCSRSQNTVCRPCGPGFYNDVVSS-KPCKPCTWCNLRSGSERKQLCT 100
    43
                                                                Loca 1
CHECRPGNGMVSRCSRSQNTVCRPCGPGFYNDVVSSKPCKPCTWCN--LRSGSERKQLCT 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----QPLDQEPGPSQTPSILTSLGSTPIIEQSTKGGIS----LPIGLIVGVTSLGLLM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ARPITVQPTEAWPRTSQGPS-----TRPV---EVPGGRAVAAILGLGLVLGLLGPLAIL 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DTTSSTDVCRPHRICSILA----IPGNASTDAVCAPESPTLSAIPRTLYVSQPEPTRS--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             --PGDNQACKPWTNCTLAGKHTLQPASNSSDAICEDRDP----PAT----QPQETQGPP 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KQQNRVCACEAGRYCALKTHSGSCRQCMRLSKCGPGFGVASSRAPNGNVLCKACAPGTFS 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CCAKCPPGQYVKHFCNKTSDTVCADCEASMYTQVWNQFRTCLSCS-SSCSTDQVETRACT 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                Similarity
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                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          --LLRRDQRLP--PD 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13.1%;
                                                             12.18; 23.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                34;
                                       Score 186.5;
Pred. No. 1.7e
25; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 201.5; DB 2
Pred. No. 2.9e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -- TQPLDSYKPG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PIDN: AAA53133.1;
                                                                                    DB
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Best Local
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                                                             186
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A; Molecule type: mRNA
A; Rolecule type: mRNA
A; Residues: 1-461 <HIM>
A; Residues: 1-461 <HIM: 9207361; PIDN: AAA42256.1; PID: 9207362
C; Comment: This protein is one of two known receptors for both TNF-alpha (cachectin C; Superfamily: tumor necrosis factor receptor; transmembrane protein F; 1-29, Domain: signal sequence #status predicted <SIG>
F; 30-461/Product: tumor necrosis factor receptor type 1 *status predicted <MAT>
F; 30-201/Product: tumor necrosis factor binding protein *status predicted <TBP>
F; 44-82/Domain: NGF receptor repeat homology <NG1>
F; 84-126/Domain: NGF receptor repeat homology <NG2>
F; 84-126/Domain: NGF receptor repeat homology <NG2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         tumor necrosis factor receptor 1 precursor - rat
N;Contains: tumor necrosis factor binding protein 1 (TNF blocking
C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Jun-1992 #sequence_revision 07-Oct-1994 #text_change 22
C;Accession: B36555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 F;212-234/Domain: transmembrane #status predicted <MEM>
F;235-461/Domain: intracellular #status predicted <INT>
F;54,151,201/Binding site: carbohydrate (Asn) (covalent) #status
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Title: Molecular cloning & A;Reference number: A36555; A;Accession: B36555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             F;127-167/Domain: NGF receptor repeat homology <NG3>F;168-204/Domain: NGF receptor repeat homology <NG4>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R;Himmler, A.; Maurer-Fogy, I.; Kroenke, M.; Scheurich, P.; Pfizenmaier, K.; Lantz, M
DNA Cell Biol. 9, 705-715, 1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                237 EEDGCSCRFPEEEE 250
164 AICEDRDPPATQPQETQGPPARPIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    253 PPGGGSFRTPIQEE 266
                                                                                                                                                                                                                                                                                                                                                                                                                    61 NTVCRPCGPGFY----NDVVSSKPCKPCTWCNLRSGSERKQL-----CTATQDTVCRC 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17 LLLGLGLSTVTGL-HCVGD------TYPSNDR-CCHECRPGNGMVSRC-SRSQ
                                                                                                                                                                                                                                                                                                                                                   78 ETVCEVCDKGTFTASQNHVRQCLSCKTC-----RKEMFQVEISPCKADMDTVCGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18 LLMGIHPSGVTGLVPSLGDREKRDNLCPQGKYAHPKNNSICCTKCHKGTYLVSDCPSPGQ 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CSNCPAG----TECDNNRNQICSPCPPNSFSSAGGQRTCDICRQCKGVFRTRKE----CS
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                                                                        KKNQECMKLCLPPVANVTNPQDSGTAVLLPLVIFLGLCLLFFICISLLCRYPQWRPRVYS
                                                                                                                                                                                                             KKNQFQRYLSETHFQCVDCSPCFNGTVTIPCKEKQNTVCNCHAGFFLSGNE--CTPCSHC
                                                                                                                                                                                                                                                                              RAG---TQPLDSYKPGVDCAP-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                            -AGKHTLQPASNSSD--
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Pred. No. 0.00025;
9; Mismatches 94
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                                                                                                                                                                                                                                                                              ----CPPGHFSPGDNQACKPWTNC
   --VQPT---EAWPRTSQGPSTRPVE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 461;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels 134;
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		Db 246 IICRDSAPVKEVEGEGIVTKPLTPASIPAFSPNPGFNPTLGFSTTPRESHPVSSTPIS 303 Qy 209VPGGRAVAAILGLG-LVLGLLGPLAI 233

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Post-processing: Minimum Match
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Perfect score:
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ALIGNMENTS

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P43489; Q13663;
01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Tumor necrosis factor receptor superfamily member 4 precursor (OX40L receptor) (ACT35 antigen) (TAX-transcriptionally activated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.

MEDLINE-94170844; PubMed-7510240;

Latza U., Duerkop H., Schnittger S., Ring

"Hummel M., Fonatsch C., Stein H.;

"The human OX40 homolog: cDNA structure,

assignment of the ACT35 antigen.";

Eur. J. Immunol. 24:677-683(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Baum P.R., Gayle R.B. III, Ramsdell F., Srinivasan S., Sorensen Watson M.L., Seldin M.F., Clifford K.N., Grabstein K., Alderson "Identification of OX40 ligand and preliminary characterization its activities on OX40 receptor.";

Circ. Shock 44:30-34(1994).

-!- FUNCTION: RECEPTOR FOR THE OX40L/GP34 CYTOKINE.
-!- SUBCELLULAR LOCATION: Type I membrane protein.
-!- SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.
-!- DATABASE: NAME-PROW; NOTE-CD guide CD134 entry;

WWW-"http://www.ncbi.nlm.nih.gov/prow/cd/cd134.htm".
InterPro; IPR001368; TNFR_c6.

Pfam; PF00020; TNFR_c6; 3.

ProDom; PD000771; TNFR_c6; 1.

SMART; SM00208; TNFR; 3.

PROSITE; PS00652; TNFR_NGFR_1; 3.

PROSITE; PS50050; TNFR_NGFR_2; 2.

Receptor; T-cell; Antigen; Glycoprotein; Transmembrane; Repeat;
                                                                                                                                                                                                                                                                          EMBL; X75962; CAA53
EMBL; S76792; AAB33
HSSP; P25942; 1CDF.
                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it use by non-profit institutions as long as its content is in no was modified and this statement is not removed. Usage by and for commercia entities requires a license agreement (See http://www.isb-sib.ch/announce or send an email to license@isb-sib.ch).
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MEDLINE=95219871; PubMed=7704935;
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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AAB33944.1;
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SIGNAL
CHAIN
                                                                                                      01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Tumor necrosis factor receptor superfamily member receptor) (OX40 antigen) (MRC OX40).
TNFRSF4 OR TXGP1L OR OX40.
Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TNR4_RAT
P15725;
                                                                                                                                                                                                                                                                                                                         Mammalia: retazoa; Chordata; Mammalia; Eucheria; Rodentia; NCBI_TaxID=10116;
modified
                                    This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the El the European Bioinformatics Institute. There are no restitute the company of the comp
                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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ilarity 100.0%;
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TUMOR NECROSIS FACTOR RECEPTOR
SUPERFAMILY MEMBER 4.
EXTRACELLULAR (POTENTIAL).
POTENTIAL.
CYTOPLASMIC (POTENTIAL).
TNFR-CYS 1.
TNFR-CYS 2.
TNFR-CYS 3 (INCOMPLETE).
TNFR-CYS 3 (INCOMPLETE).
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N-LINKED (GLCNAC. . .) (POTENTIAL)
; 49F15525941550BF CRC64;
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Pred. No. 4.1e-99;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                          Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Rat
     not
     removed.
                       long
                     There are no restrictions ng as its content is in
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e growth facto
     Usage
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     and
                                                    EMBL outstation
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                                                                                                                                                                                                           receptor.
                                                                                                                                                                                                           positive 7
                                                            a collaboration -
MBL outstation -
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RESULT 3
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ID TINA4_B
AC P47741
AC 01-FEB
DT 01-FEB
DT 16-OCT
DE TOMOT
DE TOCOPT
GN MUS MU
OC Eukary
OC Mammal
OC MAMMA
ON NCBL_T
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Best Local Sin
Matches 168;
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TRANSMEM
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CARBOHYD
SEQUENCE
                                                                                                                                                                                                                                                                                             TNR4_MOUSE STANDARD; PRT; 2
P47741;
01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence up
16-OCT-2001 (Rel. 40, Last annotation
Tumor necrosis factor receptor superfa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Signal.
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STRAIN-BALB/C;
MEDLINE-94044750;
Calderhead D.M., I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR001368; TNFR_c6. pfam; PF00020; TNFR_c6; 3. proDom; PD000071; TNFR_c6; 1. smarr; SM00208; TNFR; 3.
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PIR; S12783; S12783.
HSSP; P19438; 1EXT.
                                                                                                                              Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=10090;
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or send an email t
                                                                                                                                                                                                                                         receptor) (OX40 antigen).
TNFRSF4 OR TXGP1 OR OX40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CHAIN
                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                     Mus musculus (Mouse)
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29895
  Buhlmann
  PubMed≖8228223;
Buhlmann J.E., v
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271
                                                                                                                                                              Chordata;
Rodentia;
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POTENTIAL.
CYTOPLASMIC (POTENTIAL).
TNER-CYS 1.
TNER-CYS 3.
TNER-CYS 3 (INCOMPLETE).
TNER-CYS 4.
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Pred.
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C06465136B16E821 CRC64;
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                                                                                                                                                              Craniata; Ver
Sciurognathi;
                                                                                                                                                                                                                                                                                                         superfamily me
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No. 6.
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                                                                                                                                                                                              Vertebrata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5; DB 1;
5.5e-53;
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  Eertwegh A
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                                                                                                                                                                                              Euteleostomi;
                                                                                                                                                                                                                                                                                                         precursor (0X40L
                                                                                                                                                                    Murinae;
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MGD; MGI:104512; Tnfrs14.
InterPro; IPR001368; TNFR_c6.
( Pfam; PF00020; TNFR_c6; 3.
R ProDom; PD000771; TNFR_c6; 1.
R ProDom; SM00208; TNFR; 3.
                                                                                                                                                                        Query Match
Best Local
                                                                                                                                                               Matches
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"Cloning
T-B cell
                                                                                                                                                                                                       TRANSMEM
DOMAIN
REPEAT
REPEAT
REPEAT
REPEAT
CARBOHYD
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Gene structure and chromosomal localization of rat OX40 protein.";
Eur. J. Immunol. 25:926-930(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          [2]
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE-95255413; PubMed-7737295;
MEDLINE-95255413; Copeland N.G., Gilbert D.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@fisb-sib.ch).
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                                                                                                                                                                                                                                                                                                          Signal.
SIGNAL
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EMBL; X85214; CAA59476.1;
HSSP; P19438; 1EXT.
                                                                                                                                                                                                                                                                                  DOMAIN
                                                                                                                                                                                                                                                                                                   CHAIN
                                                                                                                                                                                                                                                                                                                                   PROSITE; PS00652; PROSITE; PS50050;
                           190
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                                                                                                                                      ALLLLGLGLS-TVTGLHCVGDTYPSNDRCCHECRPGNGMVSRCSRSQNTVCRPCGPGFYN
                                                                                                     HFSPGDNQACKPWTNCTLAGKHTLQPASNSSDAICEDRDPPATOPQETQGPPARPITVQP
KPPGGGSFRTPIQEEQADAHSTLAKI
                                                                                           EAVNYDTCKQCTQCNHRSGSELKQNCTPTQDTVCRCRPGTQPRQDSGYKLGVDCVPCPPG
                                                                                                                            ALLLLALTLGVTARRLNCVKHTYPSGHKCCRECQPGHGMVSRCDHTRDTLCHPCETGFYN
                                                          HESPGNNQACKPWTNCTLSGKQTRHPASDSLDAVCEDRSLLATLLWETQRPTFRPTTVQS
                                                                                                                                                               169;
                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          of ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         interactions.";
ol. 151:5261-5271(1993).
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TNFR_NGFR_2;
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                                                                                                                                                                                                         30153
                                                                                                                                                                      55.7%;
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                                                                                                                                                                                                   POTENTIAL.

CYTOPLASMIC (POTENTIAL).

TNER-CYS 1.

TNER-CYS 2.

TNER-CYS 3 (INCOMPLETE).

TNER-CYS 3 (INCOMPLETE).

TNER-CYS 6 (INCOMPLETE).

N-LINKED (GLCNAC...) (INCOMPLETE).

A -> G (IN REF. 2).

MW; 06E7BB4156F0D08E CRC64.
                                                                                                                                                                                                                                                                                                                          Glycoprotein;
                                                                                                                                                               20;
                                                                                                                                                            Score 857; DB
Pred. No. 2.1e
20; Mismatches
                                                                                                                                                                                                                                                                                         TUMOR NECROSIS FACTOR RECEPTOR SUPERFAMILY MEMBER 4.
                                                                                                                                                                                                                                                                                 EXTRACELLULAR
                                                                                                                                                       DB 1,
2.1e-52;
71;
                                                                                                                                                                                                                                                                                                                          Transmembrane;
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                                                                                                                                                                                                                                                                                 (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Jenkins
                                                                                                                                                                                                                      · · ) (POTENTIAL)
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                                                                                                                                                                             Length
                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         mouse
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                                                                                                                                                                                272;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         homologue
                                                                                                                                                              6
                                                                                                                                                             Gaps
                                                                           191
                                                                                                            131
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                                          251
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                          246
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TNR3_MOUSE
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TRANSMEM
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16-OCT-2001
                                                                                                            CHAIN
                                                                                                                     SIGNAL
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                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P50284;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TNR3_MOUSE
                                                                   REPEAT
                                                                                                                             Receptor;
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247 KPCWGNSFRTPIQEEHTDAHFTLAKI 272
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REPEAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Honjo T.;
"The murine lymphotoxin-beta receptor cDNA: isolation by the signal sequence trap and chromosomal mapping.";
Genomics 30:312-319(1995).
-i- FUNCTION: RECEPTOR FOR THE LYMPHOTOXIN-BETA. POSSIBLE FUNCTION
                                                                                                                                                                                                                                                                                  InterPro: IPRO01368; TNFR_c6.
pfam; PF00020; TNFR_c6; 3.
proDom; PD000771; TNFR_c6; 1.
smarr; SM00208; TNFR; 3.
                                                                                                                                                                                                                                                                                                                                                             EMBL; U29173; AAA68964.1; -.
EMBL; L38423; AAB00846.1; -.
EMBL; U30798; AAA81334.1; -.
HSSP; P25942; ICDF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=96163885;
Nakamura T., Tash
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Force W.R., Walter B.N., Browning J.L., Ware C.F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN=CVB; TISSUE-Lung;
MEDLINE=96072804; PubMed=7594541;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           entities requires a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus (Mouse)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IMMUNE DEVELOPMENT.
SUBCELLULAR LOCATION: Type I men
SIMILARITY: CONTAINS 4 THER-CYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      expression.";
Immunol. 155:5280-5288(1995).
                                                                                                                                                                                                                                                                                                                                                MGI:104875; Ltbr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation for the Swiss Institute. There are no restrictions on its Duropean Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                       PS50050;
                                                                                                                                                                                                                                      Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                           email to license@isb-sib.ch).
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40,
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TNFR_NGFR_2;
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iro K., Nazarea
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                                                                                                                                                                                                                                     Repeat;
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Matches 93
MEDLINE-99097247; I
Nakagawa N., Kinos
Nakagawa T., Higas
Morinaga T., Higas
"RANK is the essen"
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CARBOHYD
                                                                                                                                                                                                            TISSUE-Dendritic cell;

MEDLINE-98033977; PubMed-9367155;

Anderson D.M., Maraskovsky E., Billingsley W.L., Do Anderson D.M., Maraskovsky E., Billingsley W.L., Do Tometsko M.E., Roux E.R., Teepe M.C., DuBose R.F.,

Galibert L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TR11_HUMAN STANDARD; PRT; 616 AA. 09Y606; 09Y606; 16-OCT-2001 (Rel. 40, Created) 16-OCT-2001 (Rel. 40, Last sequence update) 01-MAR-2002 (Rel. 41, Last annotation update) Tumor necrosis factor receptor superfamily member 11A precursor (Receptor activator of NF-KB) (Osteoclast differentiation factor)
                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          receptor) (ODFR).
TNFRSF11A OR RANK.
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                                                                                                                                        homologue of the TNF receptor d dendritic-cell function."; ture 390:175-179(1997).
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                   7247; PubMed-9878548;
Kinosaki M., Yamaguc
Higashio K.;
    essential signaling
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                          M., Yamaguchi
K.;
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TNFR-CYS 4.
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DOMAIN REPEAT REPEAT

POTENTIAL.
CYTOPLASMIC
TNFR-CYS 1.
TNFR-CYS 2.

TUMOR NECROSIS FACTOR RECE SUPERFAMILY MEMBER 11A. EXTRACELLULAR (POTENTIAL).

RECEPTOR

DOMAIN

TRANSMEM

Disease SIGNAL

mutation

29 616

PROSITE;

PS00652; TNFR_NGFR_1; PS50050; TNFR_NGFR_2; Glycoprotein;

Transmembrane;

Repeat;

Signal; Polymorphism;

CHAIN

ProDom; PD000771; TNFK_C6; 4.
SMART; SM00208; TNFR; 4.
PROSITE: BROACE

Pfam; PF00020; TNFR_c6;

nterPro;

IPR001368; TNFR_c6

602080;

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EMBL; AF018253; AAB8
HSSP; P25942; 1CDF.
MIM; 603499; -.
MIM; 174810; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hughes A.E., Ralston S.H., Marken Wallace R.G.H., van Hul W., Whyte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                differentiation factor in osteoclastogenesis."; Biochem. Biophys. Res. Commun. 253:395-400(1998).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             s SWISS-PROT entry is copyright. It is produced through a collab
ween the Swiss Institute of Bioinformatics and the EMBL outst
European Bioinformatics Institute. There are no restrictions
by non-profit institutions as long as its content is in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DISEASE: DEFECTS IN TNFRSF11A ARE A CAUSE OF FAMILIAL PAGET DISEASE OF BONE, ALSO KNOWN AS PAGET DISEASE OF BONE 2 (PDB2). IT IS A BONE REMODELLING DISCADE MITH CLIMICAL SIMILARITIES TO FEO. UNLIKE FEO, HOWEVER, AFFECTED INDIVIDUALS HAVE INVOLVEMENT OF THE AXIAL SKELETON WITH LESIONS IN THE SPINE, PELVIS AND SKULL. SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SKELETAL MUSCLE, THYMUS, LIVER, COLON, SMALL INTESTINE AND A GLAND.

DISEASE: DEFECTS IN TNERSF11A ARE THE CAUSE OF FAMILIAL EXPAOSTEDLYSIS (FEO), A RARE AUTOSOMAL DOMINANT BONE DISORDER CHARACTERIZED BY FOCAL AREAS OF INCREASED BONE REMODELLING.

CHARACTERIZED BY FOCAL AREAS OF INCREASED BONE REMODELLING.

OSTEOLYTIC LESIONS DEVELOP USUALLY IN THE LONG BONES DURING ADULTHOOD. FEO IS OFTEN ASSOCIATED WITH EARLY ONSET DEAFNESS LOSS OF DENTITION.
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Genet. 24:45-48(2000).

FUNCTION: RECEPTOR FOR FANK LIGAND (RANKL; ALSO KNOWN AS FUNCTION: RECEPTOR FOR FANK LIGAND (RANKL; ALSO KNOWN AS OSTEOCLAST DIFFERENTIATION FACTOR OR ODF), ESSENTIAL FOR RAIMEDIATED OSTEOCLASTOGENESIS. INVOLVED IN THE REGULATION OF INTERACTIONS BETWEEN T-CELLS AND DENDETTIC CELLS.

SUBCELLULAR LOCATION: Type I membrane protein (Potential).

TISSUE SPECIFICITY: UBIQUITOUS EXPRESSION WITH HIGH LEVELS

TISSUE SPECIFICITY: UBIQUITOUS EXPRESSION WITH HIGH LEVELS
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Best Local
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01-AUG-1988 (Rel. C
16-OCT-2001 (Rel. 4
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16-OCT-2001 (Rel. 40, Last annotation update)
Tumor necrosis factor receptor superfamily member 16 precursor (Low-affinity nerve growth factor receptor) (NGF receptor) (Gp80-LNGFR)
(RP5 ICD) (Low affinity neurotrophin receptor p75NTR).
                                                                                                     Sehgal A., Patil N., Chao M.;
"A constitutive promoter directs expression of receptor gene.";
Mol. Cell. Biol. 8:3160-3167(1988).
-I- FUNCTION: LOW AFFINITY RECEPTOR WHICH CAN AND NT-4. CAN MEDIATE CELL SURVIVAL AS WEL
                                                                                                                                                     MEDLINE-89096903; Put
Sehgal A., Patil N.,
                                                                                                                                                              SEQUENCE OF 1-22 FROM N.A. MEDLINE=89096903; PubMed=2850481;
                                                                                                                                                                                          "Expression and structure of the Cell 47:545-554(1986).
                                                                                                                                                                                                            Johnson D., Lanahan A Bothwell M., Chao M.;
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                                    SUBUNIT: CAN FORM A HOMODIMER THROUGH DISULFIDE BOND INTERACTS WITH P75NTR-ASSOCIATED CELL DEATH EXECUTOR SUBCELLULAR IOTHOR: Type I membrane protein. PTM: N- AND O-GLYCOSYLATED AND IS PHOSPHORYLATED ON SIMILARITY: CONTAINS 4 THER-CYS REPEATS.
SIMILARITY: CONTAINS 1 DEATH DOMAIN.
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           SWISS-PROT entry is copyright. It is produced through a collaboration sen the Swiss Institute of Bioinformatics and the EMBL outstation
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SMART; SM00208; TNFR; 3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       162010;
                                                                                                                                                                                          VGARRLGR---GP-CAALLLLGLGL----STVTGLHCVGDTYPSNDRCCHECRPGNGMV
                                                                          QPCGANQ-TVCEPCLDSVTFSDVVSATEPCKPCTECVGLQSMSAP---CVEADDAVCRCA
                                                                                                                SRCSRSQNTVCRPCGPGF-YNDVVS-SKPCKPCTWC-NLRSGSERKQLCTATQDTVCR--
                                                                                                                                                      MGAGATGRAMDGPRLLLLLLLGVSLGGAKEACPTGL-----YTHSGECCKACNLGEGVA
YGYYQDETTGRCEACRVCEAGSGLVFSCQDKQNTVCEECPDGTYSDEANHVDPCLPCTVC
                                                                                                                                                                                                                                 84;
                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PS00652; TNFR_NGFR_1;
PS50050; TNFR_NGFR_2;
PS50017; DEATH_DOMAIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Neurogenesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   equires a license agreement (S email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                         60
427
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30.1%;
                                    -CRAGTQPLDSY -- KPGVDCAPCPPGHFSPGDNQA -- CKPWTNC
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                                                                                                                                                                                                                               31;
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BY SIMILARITY.
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Pred. No. 7.9e
31; Mismatches
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CYTOPLASMIC (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Glycoprotein; Repeat;
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nes 95;
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DTERQLRECTRWADAECEEIPGRWITRSTPPEGSDSTAPSTQEPEAPPEQDL-IASTV

-RDPPATQPQETQGPPARPITVQPTE

193

228

-VPGGRAVAAILGLGLV

224

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RA Deloukas P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R.,
RA Jones M., Stavrides G., Almeida J.P., Babbage A.K., Bagguley C.L.,
RA Bailey J., Barlow K.E., Bates K.N., Beard L.M., Beare D.M.,
RA Beasley O.P., Blrd C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,
RA Beasley O.P., Burd C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,
RA Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,
RA Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,
RA Clegg S., Cobley V.E., Collier R.E., Connor R., Corby N.R.,
RA Clusson A., Coville G.J., Deadman R., Dhami P., Dunn M.,
RA Clington A.G., Frankland J.A., Fraser A., French L., Garner P.,
RA Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,
RA Huckle E., Hunt A.R., Hunt S.E., Jakosch K., Johnson C.M., Johnson D.,
RA Hummond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,
RA Hummond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,
RA Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,
RA Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,
RA Kay M.P., Kimberley A.M., Lloyd C., Lloyd D.M., Lovell J.D.,
RA Kay M.P., Kimberley A.M., McConnachie L.J., McLay K., McMurray A.A.,
RA Milne S., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,
RA Millimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H.,
RA Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Shownkeen R., Sims S.,
RA Swann M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,
RA Wiltehead S.L., Whittaker P., Willey D.L., Walliams L., Williams S.A.,
RA Wiltehead S.L., Whittaker P., Willey D.L., Williams S.A.,
RA Milme S., San P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
RA Milme S., San P. W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
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01-MAY-1992
01-MAR-2002
                                                           "The role of polar interactions in the molecular recognit: with its receptor CD40.; with its receptor CD40.; protein Sci. 7:1124-1135(1998).

-I- FUNCTION: RECEPTOR FOR A CYTOKINE LIGAND KNOWN AS CD40-1- SUBCELLULAR LOCATION: Type I membrane protein.
-I- TISSUE SPECIFICITY: B-CELLS AND IN PRIMARY CARCINOMAS
-I- SIMILARITY: CONTAINS 4 THER-CYS REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.

MEDLINE-89356608; PubMed-2475341;

Stammenkovic I., Clark E.A., Sedd B.;

Stamphocyte activation molecule related factor receptor and induced by cytokines in EMBO J. 8:1403-1410(1989).
                                                                                                                                                                                                            3D-STRUCTURE MODELING OF 26-186 IN COMPLEX WITH CD40L. MEDLINE-98266353; PubMed-9605317; Singh J., Garber E., van Vlijmen H., Karpsusas M., Hsu Zheng Z., Naismith J.H., Thomas D.;
                                                                                                                                                                                                                                                                                                                      "Construction and analysis of a d
the ligand binding domain of the
Proteins 27:59-70(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa;
Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-97189482;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                 3D-STRUCTURE MODELING OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            tomo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CD40L receptor) (B-cell
                   DATABASE: NAME=PROW; NOTE=CD guide CD40 entry; WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd40.htm"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA sequence and comparative analysis of human re 414:865-871(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (Rel. 22, Create, (Rel. 22, Last sequence update); (Rel. 21, Last sequence update); (Rel. 41, Last annotation update) sils factor receptor superfamily member 5 preprior) (B-cell surface antigen CD40) (Bp50)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (Human).
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                                                                                                                                                                                                                                                                                                                                                                                                             PubMed-9037712;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chordata;
Primates;
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                                                                                                                                                                                                                                                                                                                                            detailed
he human B
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                                                                                                                                                                                                                                                                                                                                          three-dimensional cell receptor CD4(
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                                                                                                                            KNOWN AS CD40L
                                                                                                                                                                                            recognition
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)) (CDw40).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; X60592; CAA43045.
EMBL; AL035662; CAC1767
PIR; S04460; S04460.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Event the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entitles requires a license agreement (See http://www.isb-sorsend an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS00652; TNFR_NGFR_1; PROSITE; PS50050; TNFR_NGFR_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
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1CDF; 01-APR-97.
                                                               LVLVFIKKVAKKPTNKAPHPKQEPQEINFPDDLPGSNTAAPVQE
                                                                                                                                                                                                           P-CKPCTWCNLRSGSERKQLCTATQDTVCRCRAGTQPLD-----SYKPGVD----
                                                                                                                                                                                                                                LTAVHPEPPTACREKQYLINSQCCSLCQPGQKLVSDCTEFTECLPCGESEFLDTWNRE
                                                                                                                                                                                                                                                   VTGLH------CVGDTYPSNDRCCHECRPGNGMVSRCSRSQNTVCRPCGPGFYNDVVSSK
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                                                                                  LALYLLRRDQRLP----PDAHKPP-----GGGSFRTPIQE
                                                                                                                          QPQETQGPPARPITVQPTEAWPRTSQGPSTRPVEVPGGRAVAAILGLGLVLGLLGPLAIL
                                                                                                                                               ATGVSDTICEPCPVGFFSNVSSAFEKCHPWTSCETKDLVVQQAGTNKTDVVC-----
                                                                                                                                                                                       THCHQHKYCDPNLGLRVQQKGTSETDTICTCEEGWHCTSEACESCVLHRSCSPGFGVKQI 134
                                                                                                                                                                                                                                                                          66;
                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        B-cell; Glycoprotein;
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                                                                                                                                                                                                                                                                          Conservative
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Pred. No. 8.7e-09;
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CYTOPLASMIC
TNFR-CYS 1.
TNFR-CYS 2.
                                                                                                                                                                                                                                                                                                                           N-LINKED (GLCNAC. . .) (P
N-LINKED (GLCNAC. . .) (P
; BC8776EC2C4A5580 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                         TNFR-CYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TUMOR NECROSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EXTRACELLULAR (POTENTIAL).
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                                                                                                       GPQDR------LRALVVIPIIFGIL--FAIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Transmembrane; Repeat; Signal;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIS FACTOR RECEPTOR MEMBER 5.
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16-OCT-2001 (Rel. 40, L
01-MAR-2002 (Rel. 41, L
Tumor necrosis factor r
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TNFRSF11A OR RANK.
Mus musculus (Mouse).
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TISSUE-Fetal liver;
MEDLINE-98032977; PubMed-9367155;
MEDLINE-98032977; PubMed-9367155;
Anderson D.M., Maraskovsky E., Billingsley W.L., Donate P., DuBose R.F.,
Anderson D.M., Maraskovsky E., Teepe M.C., DuBose R.F.,
                                                                                                                                                                                                                                  DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                          PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   differentiation factor in osteoclastogenesis.";
Biochem. Biophys. Res. Commun. 253:395-400(1998).
-i- FUNCTION: RECEPTOR FOR RANK LIGAND (RANKL; ALSO KNOWN AS OSTEOCLAST DIFFERENTIATION FACTOR OR ODF), ESSENTIAL FOR MEDIATED OSTEOCLASTOGENESIS. INVOLVED IN THE REGULATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa;
Mammalia; Eutheria;
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REPEAT
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Morinaga T., Higashio K.;
"RANK is the essential signaling receptor for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "A homologue of the TNF receptor and dendritic-cell function."; Nature 390:175-179(1997).
    DISULFID
                                                                                                                                                                                                                                                                                                  CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00020; TNFR_c6; 3. ProDom; PD000771; TNFR_c6; 1. SMART; SM00208; TNFR; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MGD; MGI:1314891; Tnfrsf11a. InterPro; IPR001368; TNFR_c6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AF019046; AAB86810.1; HSSP; P25942; 1CDF.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INTERACTIONS BETWEEN T-CELLS AND DENDRITIC CELLS.
SUBCELULIAR LOCATION: Type I membrane protein (Potential).
TISSUE SPECIFICITY: UBIQUITOUS EXPRESSION WITH HIGH LEVELS IN
TRABECULAR BONE, THYMUS, SMALL INTESTINE, LUNG, BRAIN AND KIDNEY.
WEAKLY EXPRESSED IN SPLEEN AND BONE MARROW.
SIMILARITY: CONTAINS 4 TNER-CYS REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way ified and this statement is not removed. Usage by and for commercial ities requires a license agreement (See http://www.isb-sib.ch/announce/send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                             PS50050;
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    TNFR_NGFR_1; 1.
TNFR_NGFR_2; 1.
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Rodentia;

    Last annotation update)
    receptor superfamily member 11A precursor
of NF-KB) (Osteoclast differentiation factor

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Sciurognathi; Muridae;
Y SIMILARITY.
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Best Local
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P20333;
01-FEB-1991 (Rel. J
01-AUG-1991 (Rel. J
16-OCT-2001 (Rel. 4
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CARBOHYD
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SEQUENCE
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Brodeur G.M.;
"Physical mapping and gen
"Physical 35:94-100(1996)
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16-OCT-2001 (Rel. 40, Last annotation update)
Tumor necrosis factor receptor 2 precursor
binding protein 2) (TBPII) (p80) (TNF-R2) (
TNFRSFIB OR TNFR2 OR TNFBR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Smith C.A., Davis T., Anderson Dower S.K., Cosman D., Goodwin "A receptor for tumor necrosis cellular and viral proteins."; Science 248:1019-1023(1990).
                                                                                                                                                                                                                                                                                                                      Kohno T., Brewer M.T., Baker S.L., Schwartz P.E., King Hale K.K., Squires C.H., Thompson R.C., Vannice J.L.; "A second tumor necrosis factor receptor gene product naturally occurring tumor necrosis factor inhibitor."; proc. Natl. Acad. Sci. U.S.A. 87:8331-8335(1990).
                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
MEDLINE=91045991; PubMed=
Kohno T., Brewer M.T., Ba
Hale K.K., Squires C.H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa;
Mammalia; Eutheria;
                       and
                                                                             SEQUENCE OF 116-461 FROM N.A., AND MEDLINE=90349572; PubMed=2166946; Heller R.A., Song K., Onasch M.A.,
                                                                                                                                                                                                                        MEDLINE=96299745; PubMed=8661109; Beltinger C.P., White P.S., Maris J. Lepaslier D., Stallard B.J., Goeddel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. MEDLINE=90260639;
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                                                          Ringold G.M.
                                                                                                                                                                                                                                                                                    SEQUENCE
                                       "Complementary
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cad. Sci. U.S.
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y; PubMed=2160731;

T., Anderson D., Solam
Goodwin R.G.;

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    P
of a receptor for tumor form of the receptor."; A. 87:6151-6155(1990).
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Pred. No. 1.8e-08;
7; Mismatches 84
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N-LINKED (GLCNAC. . .) (P
F8C1872E99511D8E CRC64;
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Catarrhini;
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                                                                               Fischer W.H., Chang
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i; Hominidae;
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                                         for tumor necrosis
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F.J.,
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NATURE 398:535-538(1999).

NATURE 398:535-538(1999).

PERMOXIMATELY 5-FOLD LOWER AFFINITY FOR TNF-BETA.

SUBCELLULAR LOCATION: Type I membrane protein.

PTM: PHOSPHORYLATED, MAINLY ON SERINE RESIDUES WITH A VERY LOW LEVEL ON THREONINE RESIDUES.

PARAMACEUTICAL: Available under the name Embrel (Immunex and Wyeth-Ayerst). Used to treat moderate to servere rheumatoid arthritis (RA). Embrel consist of the extracellular ligand-binding portion of TNFR2 linked to an Immuglabulin Fc chain. It binds to TNFR2 linked to an Immuglabulin Fc chain. It binds to TNFR2 lipha and blocks its interactions with receptors.

SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.

PATABASE: NAME-PROW; NOTE-CD guide CD120b entry;
WWW-Thtp://www.ncbi.nlm.nih.gov/prow/cd/cd120b.htm".

DATABASE: NAME-Enbrel; NOTE-Clinical information on Embrel;
WWW-Thtp://www.enbrelinfo.com/".
                                                                             EMBL;
EMBL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Blochemical properties of the 75-kDa tumor necrosion of ligand binding, internalization, internalization, characterization.";
                                                                                                                                                                                                                                                                                                                                                        entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                distinct tumor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Two tumor necrosis factor-binding proteins purified from human urine. Evidence for immunological cross-reactivity with cell sutumor necrosis factor receptors.";
                                                                                                                                                                                                                                                                                                                   EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                  modified and this statement is not removed
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 23-40; 65-69; 136-141; 300-306 AND MEDLINE-91056048; PubMed-2173696;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 [5]
SEQUENCE OF 27-31.
MEDLINE-90110215; PubMed-2153136;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pennica D., Lam V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Purification and partial amino acid sequence distinct tumor necrosis factor receptors from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Brockhaus M.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Engelmann H., Novick D., Wallach D.;
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AAA63262.1;
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265:1531-1536(1990).
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T., Mize N.K., Weber
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HL60 cells.";
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affinity
               Tumor necrosis
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REPEAT
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PROSITE; PS50050; TNFR_NGFR_2; 4.
Receptor; Transmembrane; Glycoprotein; Repeat; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00020; TNFR_c6;
ProDom; PD000771; TNFR_c
SMART; SM00208; TNFR; 4.
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MIM; 191191;
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A23666; A23666
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                                                                                                                                                                                                         RTSQGPSTR-----PVEVPGGRAVAAILGLGLVLGL--LGPLAI
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 nerve
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growth
                factor
                                                                                               STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    48316 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14.18;
26.08;
Last sequence update)
Last annotation update;
receptor superfamily member 16 precursor (Low-
factor receptor) (NGF receptor) (Gp80-LNGFR)
                                                               Created)
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BY
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TNER-CYS 1.
TNER-CYS 2.
TNER-CYS 3.
TNER-CYS 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 217; DB 1;
Pred. No. 2.8e-08;
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                                                                                              PRT;
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-> M (IN REF. 1 AND 3).
-> T (IN REF. 4).
603B580ECD67636F CRC64;
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SEQUENCE FROM N.A. MEDLINE=87115859; Pure Radeke M.J., Misko Tensfer and r
                                                                                                                                                                                                                                                                                                                            use by modified
 DOMAIN
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DISULFID
                                                                                          DOMAIN
TRANSMEM
                                                                                                                                                                                            SMART;
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between
                               REPEAT
REPEAT
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REPEAT
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                                                                                                                                                                          PROSITE;
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EMBL; X61269; -; NOT_ANNO
PIR; A26431; A26431.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nature
[2]
                                                                                                                                                                                                                                                                                                                                                                                          -----
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Liepinsh E., Ilag L.L., Otting G., Ibanez
"NMR structure of the death domain of the
EMBO J. 16:4999-5005(1997).
-1- FUNCTION: LOW AFFINITY RECEPTOR WHICH
AND NT-4. CAN MEDIATE CELL SURVIVAL AS
NEURAL CELLS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-93077038; PubMed-1446821; Metsis M., Timmusk T., Allikmets R., Saarma M., Persson Regulatory elements and transcriptional regulation by and retinoic acid of the rat nerve growth factor recept Gene 121:247-254(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (p75
NGFR
                                                                                                                                                                                                                                  InterPro; IPR000488; Death. InterPro; IPR001368; TNFR_c6.
                                                                                                                                                                                                                                                      PDB; 1NGR;
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                                                                                                                                                                                                                                                                                                                                                  the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rattus norvegicus (
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                              REPEAT
                                                                                                                                   SIGNAL
                                                                                                                                           Phosphorylation;
                                                                                                                                                     Receptor;
                                                                                                                                                                PROSITE;
                                                                                                                                                                                                                                                                                                                   entities requires
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FISSUE=Liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                       tities requires a license agreement (See send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                    SUBUNIT: CAN FORM A HOMODIMER THROUGH DISULFIDE I SUBCELULAR LOCATION: Type I membrane protein. PTM: N- AND O-GLYCOSYLATED AND IS PHOSPHORYLATED SIMILARITY: CONTAINS 4 THER-CYS REPEATS.
SIMILARITY: CONTAINS 1 DEATH DOMAIN.
                                                                                                                                                                                          1; PF00531; death; 1.
1; PF00020; TNFR_c6; 4.
1T; SM00005; DEATH; 1.
1T; SM00208; TNFR; 3.
                                                                                                                                                                                                                                                                                                                                               European Bioinformatics Institute.
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                                                                                                                                                                                                                                                                                                                                                        SWISS-PROT entry is copyright. It is produced en the Swiss Institute of Bioinformatics and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                325:593-597(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C) (Low affinity neurotrophin receptor p75NTR).
                                                                                                                                                           PS00652; TNFR_NGFR_1; 3
PS50050; TNFR_NGFR_2; 4
PS50017; DEATH_DOMAIN;
                                                                                                                                                                                                                                                                                                                  non-profit instituted and this statement requires a license
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                                                                                                                                                     Neurogenesis;
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                                                                                                                                                                                                                                                                            NOT_ANNOTATED_CDS
                                                                                                                                          Signal;
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o T.P., Hsu C., Herz
d molecular cloning
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  251
273
425
108
1147
1189
249
249
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                                                                                                                                                                                                                                                                                                                                     institutions as long as its content
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TNFR-CYS 4.
DEATH.
SER/THR-RICH.
BY SIMILARITY
BY SIMILARITY
                                                POTENTIAL.
CYTOPLASMIC (
TNFR-CYS 1.
TNFR-CYS 2.
TNFR-CYS 3.
                                                                                                                                                                                                                                                                                                                           is not removed.
                                                                                                  TUMOR NECROSIS FACTOR RECEPTOR SUPERFAMILY MEMBER 16.
EXTRACELLULAR (POTENTIAL).
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Sciurognathi; Muridae;
                                                                                                                                                                        <u>.</u>ω
 SIMILARITY.
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                                                                                                                                           3D-structure
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                                                                                (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                  http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                L.A., Shooter E.M.;
rat nerve growth factor
                                                                                                                                                                                                                                                                                                                          Usage by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                neurotrophin receptor.";
                                                                                                                                                                                                                                                                                                                                                         and the
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                                                                                                                                                     Repeat;
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P18519;
01-NOV-1990 (Rel. 16, 0
01-NOV-1990 (Rel. 16, 1
16-OCT-2001 (Rel. 40, 1
                                                                                                                                                                                                                                                                                                                                                                                                                                               16-OCT-2001 (Rel. 40, Last sequence update)
Tumor necrosis factor receptor superfamily member 16 |
affinity nerve growth factor receptor) (NGF receptor)
(p75 ICD) (Low affinity neurotrophin receptor p75NTR).
NGFR OR TNFRSP16.
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CARBOHYD
CARBOHYD
SEQUENCE
                   SEQUENCE OF 21-416 FROM N.A.

MEDLINE-90152140; Pubmed-2154393;
Heuer J.G., Fatemie-Nainie S., Wheeler I
"Structure and developmental expression
Dev. Biol. 137:287-304(1990).
-i- FUNCTION: LOW AFFINITY RECEPTOR WHIC
                                                                                                                                                                                                                                                              MEDLINE-90166579;
                                                                                                                                                                                                                                                                                                                                                                                          Gallus gallus (Chicken).
Eukaryota; Metazoa; Chor
Archosauria; Aves; Neogn
                                                                                                                                                                "Structure and developmental expression receptor in the chicken central nervous Neuron 2:1123-1134(1989).
                                                                                                                                                                                                                              Large T.H., Weskamp G., Helde
Shooter E.M., Reichardt L.F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CHICK
                                                                                                                                                                                                                                                                                            TISSUE=Brain;
                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=9031;
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                                                                                                                                                                                                                                                                       PubMed=2560385;
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29.6%;
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; Galliformes; Phasianidae; Phasianinae;
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No. 3e-08;
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                                                              the chicken NGF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            precursor (Low-) (Gp80-LNGFR)
                                                                                                                                                                                                      growth factor
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                                                              receptor.";
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NT-4.

AFFINITY RECEPTOR WHICH CAN

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Best Local S
Matches 77
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pfam; pF00020; TNFR_C6; 4.
SMART; SM00005; DEATH; 1.
SMART; SM00005; TNFR; 3.
pR0SITE; pS50052; TNFR_NGFR_1; 3.
PROSITE; pS50017; DEATH_DOMAIN; 1.
Receptor; Neurogenesis; Transmembrane; Gl
                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
DISULFID
CONFLICT
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PIR; A60504.
HSSP; P07174; INGR.
InterPro; IPR000488; Death.
InterPro; IPR001368; TNFR_c6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIGNAL
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Phosphorylation;
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SUBUNIT: CAN FORM A HOMODIMER THROUGH DISULFIDE BOND FORMATION.

SUBCELLULAR LOCATION: Type I membrane protein.

PYM: N- AND O-GLYCOSYLATED AND IS PHOSPHORYLATED ON SERINE.

SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.

SIMILARITY: CONTAINS 1 DEATH DOMAIN.
                                                                                                                                ----PGVD-----CAPCPPGHFSPGDN--QACKPWTNCTLAGKHTLQPASNSSDAICEDR
     PGGRÄVAAILGL
                                      HPRWTTHTPSLAGSDSPEPITRDPFNTEGMATTLADIVTTVMGSSQPVVSRGTADNLIPV
                                                                                                          GLMFPCRDSQDTVCEECPEGTFSDEANFVDPCLPCTICE - ENEVMVKECTATSDAECRDL
                                                                                                                                                                               TVSATEPCKPCTQCVGLHSMSAP---CVESDDAVCRCAYGYFQDELSGSCKECSICEVGF
                                                                                                                                                                                                                VVS-SKPCKPCTWC-NLRSGSERKQLCTATQDTVCRCRAG---TQPLDSYK-----
                                                                                                                                                                                                                                                                                      LLLLGLGLSTVTGLHCVGDTYPSNDRCCHECRPGNGMVSRCSRSQNTVCRPCGPGF-YND
                                                                                                                                                                                                                                                     LLLLPAGPTWGSKEKCLTKMYTTSGECCKACNLGEGVVQPCGVNQ-TVCEPCLDSVTYSD
                                                                                                                                                                                                                                                                                                                         l Similarity
77; Conser
                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                          Signal;
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                                                                                                                                                                                                                                                                                                                                                                                                               MW;
                                                                                                                                                                                                                                                                                                                         23;
                                                                                                                                                                                                                                                                                                                                                                                                                            DEATH.

SERTHR-RICH.
BY SIMILARITY
BY SIMILA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TUMOR NECROSIS FACTOR RECEPTOR SUPERFAMILY MEMBER 16.
EXTRACELLULAR (POTENTIAL).
POTENTIAL.
CYTOPLASMIC (POTENTIAL).
THER-CYS 1.
THER-CYS 2.
                                                                                                                                                                                                                                                                                                                         Score 211.5;
Pred. No. 6e-0
23; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                               6BCEAAB54F4D2D56
                                                                                                                                                                                                                                                                                                                                        211.5; DE
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                                                                       -AWPRTSQGPSTRPVEV
                                                                                                                                                                                                                                                                                                                                                      Length
                                                                                                                                                                                                                                                                                                                       Indels
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                                                                                                                                                                                                                                                                                                                                                            416;
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                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; L04270;
HSSP; P25942;
MIM; 600979;
                                                                                                                                                                                                                                                                      Receptor;
SIGNAL
CHAIN
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DOMAIN
                                                                                                                                                                                                                                                                                                                         PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and for entities requires a license agreement (See http://www.isb-sibor send an email to license@isb-sib.ch).
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Crowe P.D., van Arsdale T.L., Walter B.N., Ware CENenfels B., Browning J.L., Din W.S., Goodwin R. "A lymphotoxin-beta-specific receptor.";
Science 264:707-710(1994).
-I-FUNCTION: RECEPTOR FOR THE LYMPHOTOXIN-BETA.
IMMUNE DEVELOPMENT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Construction and evaluation of a hncDNA library of human 12p transcribed sequences derived from a somatic cell hybrid."; Genomics 16:214-218(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00020; TNFR_c6; 4. ProDom; PD000771; TNFR_c6; 1. SMART; SM00208; TNFR; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lymphotoxin-beta receptor precursor 2 related protein) (Tumor necrosis : LTBR OR TNFCR OR TNFRSF3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P36941;
                                                                                                                                                                                                                                                     DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE-Liver;
MEDLINE-93252381; PubMed-8486360;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TNR3_HUMAN
                                                                                                                                                               REPEAT
                                                                                                                                                                              REPEAT
                                                                                                                                                                                                  REPEAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR001368; TNFR_c6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUBCELLULAR LOCATION: Type I membrane protein SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SWISS-PROT entry is copyright. It is produced through a casen the Swiss Institute of Bioinformatics and the EMBL
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                                                                                                                                                                                                                                                                                  PS00652; TNFR_NGFR_1; 2.
PS50050; TNFR_NGFR_2; 3.
PS50050; TNFR_NGFR_2; 3.
PTansmembrane; Glycoprotein;
1 30 POTENTIAL.
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Primates;
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CYTOPLASMIC
TNFR-CYS 1.
TNFR-CYS 2.
TNFR-CYS 3.
                                                                                                                                             TNFR-CYS
                                                                                                                                                                                                                                                     EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                      LYMPHOTOXIN-BETA RECEPTOR
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⟨ SIMILARITY.
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01-CCT-1996 (Rel. 34, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
Tumor necrosis factor receptor superfamily memb
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DISULFID
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SEQUENCE
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P27512;
01-AUG-1992
                                                                                                                                                                                       SEQUENCE FAVA. ..... SEQUENCE: STRAIN-BALB/C; TISSUE-Liver; STRAIN-BALB/C; TISSUE-Liver; MEDLINE-93994586; PubMed-1281194; MCDLINE-93994586; PubMed-1281194; MCDLINE-9394586; PubMed-1281194; MCDLINE-9394586; MCDLINE-939486, MCDLI
                                                                                                                                                                                                                                                                                                                                                                                        "Differential increase of an a species of murine CD40 upon B J. Immunol. 148:620-626(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus (Mouse)
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                      This
                                                                                                                                                                       Grimaldi J.C., Torres R., Kozak Howard M., Cockayne D.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOUSE
                    between
                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN=BALB/C; TIS
                                                                                                                                                                                                                                                                            [3]
                                                                                                                                                                                                                                                                                               Submitted (SEP-1996)
                                                                                                                                                                                                                                                                                                                                   STRAIN-BALB/C;
                                                                                                                                                                                                                                                                                                                                                      REVISIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. MEDLINE=92105763;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=10090
                                                                                                                                                  doward M., Cockayne D.A.; Genomic structure and chromosomal mapping
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         238
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                                                                                                                                      Immunol.
                                                                           SUBCELLULAR LOCATION: Type I membrane prosimilarity: CONTAINS 4 TNFR-CYS REPEATS.
                                                                                                                  mmunol. 149:3921-3926(1992).
FUNCTION: RECEPTOR FOR A CYTOKINE LIGAND
                                    SWISS-PROT entry is
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PSLCRKLGSLLKRRPQGEGPN---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VQPTEAWPRTSQGPSTRPVEVPGGRAVAAILGLGLVLGLLGPLAILLAL-----
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                                                                                                                                                                                                                                                                                                               R.M.;
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                    the
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Bioinformatics
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                      Institute
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Rodentia;
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                  copyright. It is produced through a collaboration tute of Bioinformatics and the EMBL outstation -
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Sciurognathi; Muridae
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No. 8.6e-08;
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0) (CDw40).
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restrictions
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RESULT 14
TNR9_MOUSE
ID TNR9_M
AC P20334
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DT 01-FEB

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TNR9_MOUSE P20334; 01-FEB-1991 01-FEB-1991

(Rel.

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REPEAT
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REPEAT
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EMBL; M94126; AAA37404.1;
EMBL; M94129; AAA37404.1;
EMBL; M94128; AAA37404.1;
                                                                                                                                                                                                                                                                                                                                                                                                             CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro: IPR001368; TNFR_c6.
Pfam; PF00020; TNFR_c6; 4.
ProDom; PD000771; TNFR_c6; 1.
SMART; SM00208; TNFR; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MGD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PIR;
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SIGNAL
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204
                227
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, M94127; AAA37404.1;
A46476; A46476.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MGI:88336; Tnfrsf5
IL--ITIFGVFLYIKKVVKKPKDNEMLPPAARRQDPQEMEDYPGHNTAAPV
                                                                                                                                                                    VTGLH-----CVGDTYPSNDRCCHECRPGNGMVSRCSRSQNTVCRPCGPGFYNDVVSSK
                LLGPLAILLALYLLRRDQRLPPDAHKPPGGGSFRTPIQEEQADAHSTLAKI
                                                                         ATETTDTV---
                                                                                                             IRCHQHRHCEPNQGLRVKKEGTAESDTVCTCKEGQHCTSKDCEACAQHTPCIPGFGVMEM
                                                                                                                                                  LTAVHLGQCVTCSDKQYLHDGQCCDLCQPGSRLTSHCTALEKTQCHPCDSGEFSAQWNRE
                                                      EDRDPPATQPQETQGPPARPITVQPTEAWPRTSQGPSTRPVEVPGGRAVAAILGLGLVLG
                                                                                           -TQPLDSYKPGVDCAPCPPGHFSPGDNQA · · · - - - CKPWTNCTLAGKHTLQPASNSSDAIC
                                                                                                                              -PCKPCTWCNLRSGSERKQLCTATQDTVCRCRAG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P25942;
                                                                                                                                                                                        64;
                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                        ; PS00652;
; PS50050;
                                                                                                                                                                                                                                                                                                                                                                                                                               B-cell;
                                                                                                                                                                                                                                                                                                                                          20
194
216
25
61
104
                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1CDF.
                                                                                                                                                                                                                                      ₽,
                                                                        --CHPCPVGFFS--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 it institutions as long statement is not removed a license agreement (See to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                             Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                       TNFR_NGFR_1; 1.
TNFR_NGFR_2; 4.
                                                                                                                                                                                                                                                          193
215
289
289
103
1144
187
187
197
103
1103
1103
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32111
                                                                                                                                                                                                 13.6%;
                                                                                                                                                                                                          .68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           JOINED:
JOINED:
                                                                                                                                                                                                                                      W.
                                                                                                                                                                                        39;
                                                                                                                                                                                                                                   TNFR-CYS 4.
BY SIMILARITY.
OF LINKED (GLCNAC...)
                                                                                                                                                                                                                                                                                                                                                             POTENTIAL.
CYTOPLASMIC
TNFR-CYS 1.
                                                                                                                                                                                                                                                                                                                                          TNFR-CYS
                                                                                                                                                                                                 Score 209;
Pred. No. 6
                                                                                                                                                                                                                                                                                                                                                                                         EXTRACELLULAR
                                                                                                                                                                                                                                                                                                                                                                                                    SUPERFAMILY MEMBER
                                                                                                                                                                                                                                                                                                                                                                                                             TUMOR NECROSIS
                                                                                                                                                                                                                                                                                                                                                                                                                     POTENTIAL.
                                                                         NQSSLFEKCYPWTSCEDKNLEVLQKGTSQTNVIC
                                                                                                                                                                                                                                                                                                                                                                                                                              Transmembrane;
                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (See
                                                                                                                                                                                                 DB.
                                                                                                                                                                                                                                                                                                                                                                       (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          . Usage by and for commercial http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                          (POTENTIAL).
                                                                                                                                                                                                 -08
                                                                                                                                                                                                                                                                                                                                                                                                             FACTOR
                                                                                                                                                                                        96;
                                                                                                                                                                                                                                                                                                                                                                                                                             Repeat; Signal.
                                                                                                                                                                                                                                      CRC64;
                                                                                                                                                                                                          Length
                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                               (POTENTIAL)
                                    MRALLVIPVVMG
                                                                                                                                                                                                           289;
                 277
252
                                                                                                                                                                                        92;
                                                                                                                                                                                        Gaps
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                                                                         186
                                                                                          166
                                                                                                             134
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CARBOHYD
CARBOHYD
SEQUENCE
                                                 REPEAT
REPEAT
REPEAT
                                                                                       TRANSMEM
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kwon B.S., Kozak C.A., Kim "Genomic organization and cantigen 4-1BB.";
                                                                                                                                                                           PROSITE;
                                                                                                                                                                                                                                                             EMBL; J04492; AAA40167.1;
EMBL; U02567; AAA93113.1;
PIR; B32393; B32393.
                                                                                                                                                                                                                                                                                                               use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send am email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    function.";
J. Immunol. 150:771-781(1993).
-I- FUNCTION: RECEPTOR FOR THE PUTATIVE CYTOKINE 4-1BBL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CHARACTERIZATION, AND SEQUENCE OF 25-29. MEDLINE-93139510; PubMed-7678621;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16-OCT-2001 (Rel. 40, Last annotation update)
Tumor necrosis factor receptor superfamily memb
ligand receptor) (T-cell antigen 4-1BB) (CD137
TNFRSF9 OR ILA OR LY63 OR CD137 OR CD157.
                                       REPEAT
                                                                                                                                       CHAIN
                                                                                                                                                                                                  Pfam; PF00020; TNFR_c6; SMART; SM00208; TNFR; 2.
                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN the European Bioinformatics Institute. There are no resti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "cDNA sequences of two inducible T-cell genes."; Proc. Natl. Acad. Sci. U.S.A. 86:1963-1967(1989)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. MEDLINE-89184547; PubMed-2784565;
                                                                                                               DOMAIN
                                                                                                                                                    SIGNAL
                                                                                                                                                                                                                           MGD; MGI:1101059; Tnfrsf9.
Interpro; IPR001368; TNFR_c6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kwon B.S.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pollok K.E., Kim Y.-J., Zhou Z., Hurtado J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-94179805;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM
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W
On
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Inducible T cell antigen 4-1BB. Analysis of expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ω
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                                                                                                                                                                                                                                                                                                                                                                                                                            SUBCELLULAR LOCATION: Type I membrane pr
TISSUE SPECIFICITY: EXPRESSED ON THE SUR
INDUCTION: OPTIMAL BY PMA AND IONOMYCIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACTIVE DURING T CELL ACTIVATION. SUBUNIT: PRINCIPALLY AN HOMODIMER,
                                                                                                                                                                                                                                                                                                                                                                                                                  SIMILARITY: CONTAINS 4 THER-CYS REPEATS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ASSOCIATES WITH P56-LCK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             B.S., Weissman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sequences of two
                                                                                                                                                                                                                                                    P25942;
                                                                                                                                                                        PS50050; TNFR_NGFR_1;
                                                                                                                                                               Glycoprotein;
25
188
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86
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128
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256
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                                                                     TUMOR NECROSIS FACTOR RECEP'
SUPERFAMILY MEMBER 9.
EXTRACELLULAR (POTENTIAL).
POTENTIAL.
CYTOPLASMIC (POTENTIAL).
TNER-CYS 1.
TNFR-CYS 3.
TNFR-CYS 4.
N-LINKED (GLCNAC. . .) (POTENTIAL)
N-LINKED (GLCNAC. . .) (POTENTIAL)
N-LINKED (GLCNAC. . .) (POTENTIAL)
93A10D03C60813C4 CRC64;
                                                              TNFR-CYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sciurognathi;
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                                                                                                                                                                         1.
FALSE_NEG
                                                                                                                                                               Signal; Transmembrane
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                                                                                                                                       NECROSIS FACTOR RECEPTOR
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localization
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                                                                                                                                                                                                                                                                                                                                                                                                                                         e protein.
SURFACE OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        member 9 precursor (4-1BB
0137 antigen).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           of.
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RESULT
TR1B_MC
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Best Local
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                                                                                                                                                                                                      "Cloning
                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAY-1992 (Rel. 22, Created)
01-MAY-1992 (Rel. 22, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Tumor necrosis factor receptor 2 precursor (TINFRSF1B OR TNFR2 OR TNFR-2.
                                                                                     Kissonerghis M., Fellowes R., Submitted (MAY-1995) to the El
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOUSE
                                                                                                                                         Jacob C.O.,
Submitted (
                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. MEDLINE=91246168; PubMed=1645445;
                                                                                                                                                                                                                                                                                           specific
                                                                                                                                                                                                                                                                                                         necrosis
                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P25119; P97893;
                      between
                                                                                                            TISSUE-Liver;
                                                                                                                      SEQUENCE OF 1-22 FROM
                                                                                                                                                              STRAIN-NOD;
                                                                                                                                                                         SEQUENCE OF
                                                                                                                                                                                                                                                                                                                                           Lewis
                                                                                                                                                                                                                                                                                                                                                    MEDLINE-91187885; PubMed-1849278;
                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TR1B_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 237
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                                                   FUNCTION: RECEPTOR FOR THE ALPHA.
SUBCELLULAR LOCATION: Type I membrane pr
SIMILARITY: CONTAINS 4 THER-CYS REPEATS.
          s SWISS-PROT entry is copyright. It is produced through a collab
ween the Swiss Institute of Bioinformatics and the EMBL outst
European Bioinformatics Institute. There are no restrictions
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                                                                                                                                                                                                                                                                                                                              M., Tartaglia L.A., Lee
S.H., Chen E.Y., Goeddel
                                                                                                                                                                                                                                                                                    Natl. Acad. Sci. U.S.A. 88:2830-2834(1991)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     64:
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64; Conservative
                                                                                                                                                                                                                                                                                                                     and expression of cDNAs for two
                                                                                                                                                                                               s for tumor
L. Biol. 11:
                                                                                                                                                                                                                                                                                                         factor receptors demonstrate
non-profit
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(JAN-1996)
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                                                                                                                                                                          FROM
                                                                                                                                                                                                11:3020-3026(1991).
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Rodentia;
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Pred.
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                                                                                                Feldmann
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                                                                                                                                                                                                                                                                                                                                                                                                                                       2 precursor (TNF-R2)
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No. 1.6
long
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  as
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  its
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                       EMBL outstation
                       a collaboration
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Best Local Similarity 25...
Matches 68; Conservative
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CARBOHYD
SEQUENCE
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DOMAIN
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DISULFID
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Pfam; PF00020; TNFR_C6; 4.
ProDom; PD000771; TNFR_C6; 1.
SMART; SM00208; TNFR; 4.
PROSITE; PS00652; TNFR_NGFR_1; 2.
PROSITE; PS50050; TNFR_NGFR_2; 3.
Receptor; Transmembrane; Glycoprotein; Repeat; Signal.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                           172
                                                                                                                                                                                                  134
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276
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                                     234 LLALY---------LLRRDQRLP--PD 249
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                                                                                                                                                                                                                                                                                                                                                           42
                                                                                                                                                                                                                                                                                                                                         CCHECRPGNGMVSRCSRSQNTVCRPCGPGFYNDVVSSKPCKPCTWCNLRSGSERKQL--C
                                                                                                                 PARPITVQPTEAWPRTSQGPS-----TRPV---EVPGGRAVAAILGLGLVLGLLGPLAI 233
                                                                                                                                                                                                                                                                                                                TKQQNRVCACEAGRYCALKTHSGSCRQCMRLSKCGPGFGVASSRAPNGNVLCKACAPGTF
                                                                                                                                                                                                                                                                           TATQDTVCRCRAG-----TQPLDSYKPG------VDCAPCPPGHF 133
MLGLVNCIILVQRKKKPSCLQRDAKVPHVPD
                                                                                                                                                         SDTTSSTDVCRPHRICSILA----IPGNASTDAVCAPESPTLSAIPRTLYVSQPEPTRS-
                                                                            -----QPLDQEPGPSQTPSILTSLGSTPIIEQSTKGGIS----LPIGLIVGVTSLGLL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              119 B
1127 B
1145 B
163 B
181 B
181 B
189 N
195 N
195 N
195 N
195 N
                                                                                                                                                                                                                                                                                                                                                                                             13.2%; Score 202.5; DB 1; 25.1%; Pred. No. 2.8e-07; Live 36; Mismatches 86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TNER-CYS 4.

BY SIMILARITY.

B
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TNFR-CYS
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306
                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 474;
                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                               81;
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                                                                            275
                                                                                                                                                           226
                                                                                                                                                                                                                                                                                                                                                                                               14;
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Search completed: June 18, 2002, 14:28:29 Job time: 223 sec

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Title:
Perfect score:
Sequence:
                                                                                                                                                                                                                Result
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length: 2000000000
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1: sp_archea:*
2: sp_bacteria
3: sp_fund::*
4: sp_human:*
5: sp_inverteb
6: sp_mammal:*
7: sp_mhc:*
8: sp_organel:
9: sp_plant:*
10: sp_plant:*
11: sp_rodent:
                                                                                                                                                                                                   Query
Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        June 18, 2002, 14:24:01; Search time 26.53 Seconds (without alignments) 1806.242 Million cell updates/sec
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114.7
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1538
1 MCVGARRLGRGPCAALLLLG.....SFRTPIQEEQADAHSTLAKI
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Listing first 45 summaries
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Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                            sp_unclassified:*
sp_rvirus:*
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sp_archeap:*
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I O99NEI
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                                                                                                                                                                                                     IJ
                                                                                                                                                                                                                                         SUMMARIES
         O02764 oryctolagus
O93dd2 gallus gall
O95407 homo sapien
Q16042 homo sapien
Q16042 homo sapien
O920w1 mus musculu
O99ne0 mus musculu
O91zm6 rattus norv
O9prg7 xenopus lae
O99ke0 rattus norv
O62327 mus musculu
Q96j31 homo sapien
O99ne1 mus musculu
O99ne2 mus musculu
                                                                                                                                                                                                     Description
O88734 mus musculu
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45	44	43	42	41	40	39	38		36		34	33	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17
147.5	147.5	149.5	150.5	151	151.5	151.5	152	152.5	154	155.5	157.5	157.5	157.5	157.5	158.5	160.5	162	164.5	167.5	171	171	171	173	174	178	181.5	181.5	182.5
9.6	9.6	9.7	9.8		9.9	9.9	9.9		10.0	•	•	•	10.2	10.2	10.3	10.4	10.5	10.7	10.9	11.1	11.1	11.1	11.2		11.6	11.8	11.8	11.9
348	348	349	320	401	320	320	401	316	655	186	655	655	655	186	438	372	186	186	651	461	461	327	203	401	387	430	203	430
12	12	12	12	11	12	12	11		4	12	1	1	11	12	13	4	12	12	13	11	11	Η	11	4	13	4	4	4
057103	057277	Q89118	057079	008712	057091	057300	008727	057092	075509	Q911R5	Q91W77	Q91XH9	Q9EPU5	Q9WJB4	Q9DFV0	Q9UHP4	Q9YP87	072735	Q98SM6	Q91V30	Q91Y93	Q9DCQ1	Q99NE3	000300	Q9PVD4	Q96JU1	Q9BYU0	Q969Z4
O57103 monkeypox v	057277 monkeypox v	Q89118 variola vir	057079 cowpox viru	008712 mus musculu	057091 ectromelia	O57300 ectromelia			3	0911r5 vaccinia vi	mus	Q91xh9 mus musculu	Q9epu5 mus musculu		Q9dfv0 brachydanio		Q9yp87 cowpox viru	cowpox	Q98sm6 gallus gall		Q91y93 rattus norv	Q9dcq1 mus musculu	Q99ne3 mus musculu	000300 homo sapien	Q9pvd4 xenopus lae	Q96jul homo sapien	homo	Q969z4 homo sapien

ALIGNMENTS

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ADD DATE OF THE DARK SQUARE SQ
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002764
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002764; PREMBLrel. 04, Created)
01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-DEC-2001 (TrEMBLREL. 19, Last annotation update)
        CHAIN
SEQUENCE
                                                                                   Signal.
NON_TER
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-CHBB:HM;
Isono T., Seto A.;
Isono T., Seto A.;
"Expression of OX40 and OX40 ligand genes in rabbit HTLV-I-transformed T cell lines.";
Submitted (MAY-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; AB003911; BAA20059.1; -.
HSSP; P25942; ICDF.
InterPro; IPRO1368; TNFR_C6.
                                                                                                                                                                                                            PROSITE;
                                                                                                                                                                                                                                                                                   Pfam; PF00020; TNFR_c6; 3. ProDom; PD000771; TNFR_c6; 1. SMART; SM00208; TNFR; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Oryctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OX40 PRECURSOR (FRAGMENT)
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                                                                                                                                                                                                        PS00652; TNFR_NGFR_1; PS50050; TNFR_NGFR_2;
            267 AA;
                                                      19
19
1
18 POTENTIAL.
267 OX40.
28489 MW; A8B4CD3173C9500B CRC64;
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15 ALLLLGLGLSTVTGLHCVGDTYPSNDRCCHECRPGNGMVSRCSRSQNTVCRPCGPGFYND 74

Query Match 60.1 Best Local Similarity 67.3 Matches 177; Conservative

60.1%; Score 924; DR 67.3%; Pred. No. 6.66 tive 23; Mismatches

DB 6; Length 267; i.6e-77; es 59; Indels

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Gaps

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Best Local
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ProDom; PD000//...

SMART; SM00208; TNFR; 3.

SMART; SM00208; TNFR_NEFR_2; 3.

PROSITE; PS50050; TNFR_NEFR_2; 3.

PROSITE; PS50050; TNFR_NEFR_2; 3.

PROSITE; PS50050; TNFR_NEFR_2; 3.
                                                                                                                                                                                                                                                                                                                                                  Tregaskes C.A.;
Thesis (2001), University of Reading,
Thesis (2901), University of Reading,
HSBP; P25942; ICDF.
HSSP; P25942; ICDF.
InterPro; IPR001005; Myb_DNA_bind.
InterPro; IPR001368; TNFR_C6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gallus gallus (Chicken).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAR-2001
01-DEC-2001
                                                                                                                                                                                                                                                                                                                                Pfam; PF00020; TNFR_c6; 3. ProDom; PD000771; TNFR_c6; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=9031;
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OPEE--
                     QPTEAWPRTSQGPSTRPVEVP-----GGRAVA
                                            TSDVICESSRRSSLSVLIPITAAVVTCLVGICIYCLVHTDLRRRGPKQAEAEAPRELVTQ
                                                                    SSDATCEDRDP---
                                                                                        NEPCKQGFGFVAAMAEARMTSPCEPCAEGTFSNVSSKTEPCHFWTSCEEKGLVVKVKGTN
                                                                                                                                                                                               RLGRGPCAALLLLGLGLSTVTGLHCVGDTYPSNDRCCHECRPGNGMVSRCSRSQNTVCRP
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                                                                                                                                                           CGPGFY-NDVVSSKPCKPCTWCNLRSGSERKQLCTATQDTVCRCRAGTQPLDS-----
                                                                                                                                                                                RLGLLGLLCALLLGCG-QPGDAVNCSDKQYEHKGRCCNRCQPGKKLASECNDTEDSVCTP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Metazoa;
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                                                                                                                                                                                                                              Conservative
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Neognathae; Galliformes; Phasianidae; Phasianinae;
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27.18;
VDFPVQETLLGGQPVA
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Last sequence update)
Last annotation updat
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Pred. No. 2.
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261
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ORESULT OF SOLUTION OF SOLUTIO
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                                                                                                                                                                                                                                                                                                                                         EMBL;
EMBL;
EMBL;
EMBL;
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MEDLINE-2012600; PubMed-10655513;

Bai C., Connolly B., Metzker M.L., Hilliard C.A., Liu
Bai C., Connolly B., Liu Q., Austin C.P., Caske
Soderman A., Galloway S.M., Liu Q., Austin C.P., Caske
"Overexpression of M68/DcR3 in human gastrointestinal
"Overexpression of M68/DcR3 in human gastrointestinal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=99253915; PubMed=10318773;
Yu K.Y., Kwon B., N1 J., Zhai Y., Ebner R., Kwon B.S
"A newly identified member of tumor necrosis factor
superfamily (TR6) suppresses LIGHT-mediated apoptosi
J. Blol. Chem. 274:13733-13736(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           O95407;
01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DECOY RECEPTOR 3 (M68) (M68C) (M68E) (DJ583P15.1.1)
FACTOR RECEPTOR SUPERPAMILY, MEMBER 6B, DECOY).
DCR3 OR TR6 OR TNFRSF6B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL;
                                                        SMART; SM00208; THFR; 3.

PROSITE; PS01186; EGF_2; UNKNOWN_1

PROSITE; PS00652; THFR_NGFR_1; UNKI

PROSITE; PS50050; THFR_NGFR_2; 2.
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MEDLINE-99087326; PubMed-9872321;
Pitti R.M., Marsters S.A., Lawren
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          095407
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cluster."
                                                                                                                                                                                             rram; Pr00020; TNFR_c6; 4.
ProDom; PD000771; TNFR_c6; 1.
                                                                                                                                                                                                                                                                      InterPro; IPR000561; EGF-like.
InterPro; IPR001368; TNFR_c6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (NOV-2001) to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Strausberg R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-99253915;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE-BLOOD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                  L; AF104419; AAD03056.1;
AF134240; AAD29688.1;
L; AF217796; AAF23585.1;
L; AF217793; AAF33685.1;
AF217794; AAF33686.1;
L; AL121845; CAC03668.1;
L; BC017065; AAH17065.1;
L; BC017065; AAH17065; AAH17065;
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   F90AEE33718449AF CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                              Receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00020; TNFR_C6; 4.
ProDom; PD000771; TNFR_C6; 1.
SMART; SM00208; TNFR; 4.
PROSITE; PS00652; TNFR_NGFR_1
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Cytokine 2:231-237(1990).
EMBL; S63368; AAB19824.2; -.
HSSP; P25942; ICDF.
                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
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Brockhaus M., Lesslauer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=91370690; PubMed=1966549; Dembic Z., Loetscher H., Gubler U.,
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                                                                                           TREQURICTCRPGWYCALSKQEGCRLCAPLRKCRPGFGVARPGTETSDVVCKPCAPGTFS
                                                                                                                                          TATQDTVCRCRAG---
                                                                                                                                                                                       CCSKCSPGQHAKVFCTKTSDTVCDSCEDSTYTQLWNWVP--ECLSCGSRCSSDQVETQAC
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NTTSSTDICRPHQICNVVA----IPGNASMDAVC----TSTSPTRSMAPGAVHLPQPVS
                                          --PGDNQACKPWTNCTLAGKHTLQPASNSSDAICEDRDPPATQPQETQGPPA----RPIT
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TNFR_NGFR_2;
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27.08;
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Pred. No. 6.5e-13;
                                                                                                                                                                                                                                                                                   pred. No. 7.8

mismatches
                                                                                                                                                                                                                                                                                                         Score 216;
Pred. No. 7
                                                                                                                                          -TQPLDSYKPG-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pan Y.C., Lahm
                                                                                                                                                                                                                                                                                                         DB 4;
.8e-12;
                                                                                                                                                                                                                                                                                     ; 88
                                                                                                                                                                                                                                                                                                                             Length 425;
                                                                                                                                                                                                                                                                                                                                                                                                       CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 300;
                                                                                                                         ----VDCAPCPPGHFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
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                                                                                                                                                                                                                                                                                   54;
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185
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Best Local
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Q9Z0W1;
Q1-MAY-1999
Q1-MAY-1999
Q1-DEC-20Q1
                                                                                                                                                                                                                                                                                                                                               Receptor.
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                  PROSITE;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              U1-MAY-1999 (TrEMBLrel. 10, C
01-MAY-1999 (TrEMBLrel. 10, L
01-DEC-2001 (TrEMBLrel. 19, L
NERVE GROWTH FACTOR RECEPTOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00531; death; 1.
Pfam; PF00020; TNFR_C6; 4.
SMART; SM00005; DEATH; 1.
SMART; SM00208; TNFR; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MGD; MGI:97323; Ngfr.
InterPro; IPR000488; Death.
InterPro; IPR000561; EGF-11ke.
InterPro; IPR000734; Lipase.
InterPro; IPR001368; TNFR_C6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tuffereau C., Benejean J., Blondel D., Kieffer B., Flamand A., "Low-affinity nerve-growth factor receptor (P75NTR) can serve receptor for rables virus.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AF105292; AAD17943.1; -. HSSP; P07174; 1NGR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBO J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NGFR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=99077793; PubMed=9857182;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                      PROSITE;
                                  243
                                                           209
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                                                                                                                                                                                                         DVVS-SKPCKPCTWC-NLRSGSERKQLCTATQDTVCRCRAGTQPLDSY-----
                                                                                                                                                                                                                                               LLLLGLGLSTVTGLH-CVGDTYPSNDRCCHECRPGNGMVSRCSRSQNTVCRPCGPGF-YN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TRSQHTQPTPEPSTAPSTSFLLPMGPSPPAEGSTGDFALPVGLIVGVTALGLLII
                                  NLIPVYCSILAAVVVGLV
                                                          -- VPGGRAVAAILGLGLV 224
                                                                                                                                  SGLVFSCQDKQNTVCEECPEGTYSDEANHVDPCLPCTVCE-DTERQLRECTPWADAECEE
                                                                                                                                                                                  DVVSATEPCKPCTECLGLQSMSAP----CVEADDAVCRCSYGYYQDEETGRCEACSVCGVG
                                                                                                                                                                                                                                   LLLLLLGVSFGGAKETCSTGMYTHSGECCKACNLGEGVAQPCGANQ-TVCEPCLDSVTFS
                                                                                  IPGRWITRSTPPEGSDVTTPSTQEPEAPPERDL-IASTVADTVTTVMGSSQPVVTRGTAD
                                                                                                                                                                                                                                                                                 1 Similarity
78; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17:7250-7259(1998).
                                                                                                                                                                                                                                                                                                                                                                 PS50017; DEATH_DOMAIN; 1.
PS00186; EGF_2; UNKNOWN_1.
PS00120; LIPASE_SER; UNKNOWN_1.
PS00652; TNFR_NGFR_1; 3.
PS50050; TNFR_NGFR_2; 4.
                                                                                                   ----RDPP----ATQP--QETQGPPARPITVQPTEAWPRTSQGPSTRPVE-----
                                                                                                                                                                                                                                                                                                                                               417
                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                        -KPGVDCAPCPPGHFSPGDNQA--CKPWTNCTLAGKHTLQPASNSSDAICED
                                                                                                                                                                                                                                                                                                                                               ĀΑ;
                                                                                                                                                                                                                                                                                                                                               44686 MW;
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Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Created)
                                                                                                                                                                                                                                                                                             Score 212.5; DB 1
Pred. No. 1.6e-11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sciurognathi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                               5D7A4510DB8AF9B2 CRC64;
                                                                                                                                                                                                                                                                                  Mismatches
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                                                                                                                                                                                                                                                                                  98;
                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                       Length 417;
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RESULT

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Best Local S
Matches 59
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O99NEO;
O1-JUN-2001 (TrEMBLrel. 17
? 01-JUN-2001 (TrEMBLrel. 1:
T 01-DEC-2001 (TrEMBLrel. 1:
Tran Type V ISOFORM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-21117110; pubMed-11172023; Tone M., Tone Y., Fairchild P.J., Wyke "Regulation of CD40 function by its 1s alternative splicing."; Proc. Natl. Acad. Sci. U.S.A. 98:1751-EMBL; AJ401390; CAC29430.1; -. HSSP, P25942; ICDF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Prodom; PD000771; TNFR_c6; 1.

SMART; SM00208; TNFR; 4.

PROSITE; PS00037; MYE 1; UNKNOWN_1.

PROSITE; PS00962; RIBOSOMAL_S2_1; UN PROSITE; PS00652; TNFR_NGFR_1; 1.

PROSITE; PS50050; TNFR_NGFR_2; 4.

PROSITE; PS50050; TNFR_NGFR_2; 4.

SEQUENCE 260 AA; 28895 MW; 57A5B
                                                                                                                                                                                                                             O91ZM6;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
TUMOR NECROSIS FACTOR RECEPTOR TYPE II (FRAGMENT).
STRAIN-SPRAGUE-DAWLEY;
Osburg B., Peiser C., Doemling D., Schomburg L., Voigt K.,
"TNF-receptors p60 and p80 are constitutively expressed by
capillary endothelial cells and participate in TNF-alpha tr
                                                                                                    SEQUENCE FROM N.A
                                                                                                                                                                  Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                               Rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                          NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         187
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LTAVHLGQCVTCSDKQYLHDGQCCDLCQPGSRLTSHCTALEKTQCHPCDSGEFSAQWNRE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EKVVKKPKDNEMLPPAARRQDPQEMEDYPGHNTAAPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -TQPLDSYKPGVDCAPCPPGHFSPGDNQA-----CKPWTNCTLAGKHTLQPASNSSDAIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IRCHQHRHCEPNQGLRVKKEGTAESDTVCTCKEGQHCTSKDCEACAQHTPCIPGFGVMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -PCKPCTWCNLRSGSERKQLCTATQDTVCRCRAG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pro; IPR001005; Myb_DNA_bind.
Pro; IPR001865; Ribosomal_S2.
Pro; IPR001368; TNFR_c6.
PF00020; TNFR_c6; 4.
                                                                                                                                                                                                               norvegicus
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llarity 27.2%;
Conservative 2
                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -CHPCPVGFFS----NQSSLFEKCYPWTSCEDKNLEVLQKGTSQTNVIC
                                                                                                                                                                                                               (Rat)
                                                                                                                                                                    Chordata;
Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17,
17,
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Pred. No. 1.2e
27; Mismatches
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Last annotation update)
                                                                                                                                                               Craniata; Vertebrata;
Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Craniata; Vertebrata; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        98:1751-1756(2001).
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57A5BACE8CF2F546 CRC64;
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ts isoforms
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ns generated
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length
                                                                                                                                                                  Euteleostomi;
; Murinae; Rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Euteleostomi;
; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   through
                       Bickel U.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus
                                                                                                                                                                    Rattus
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RESULT
Q9PRG7
                                                                                                                                                                                                                                                                                                                                                                                                                               Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                   В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    δ
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                                                                                                                                                                                                                                                                                                                                                                                                                В
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local S
Matches 68
Query
                                                            P75NTRA.

Xenopus laevis (African clawed frog).

Chordata; Craniata;
                                                                                                                                                                                                                                                                                    O9PRG7:
01-mAY-2000 (TrEMBLrel. 13,
01-MAY-2000 (TrEMBLrel. 13,
01-JUN-2001 (TrEMBLrel. 17,
P75 NEUROTROPHIN RECEPTOR A-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         through the blood-brain barrier.";
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ
EMBL; AF420214; AAL16021.1; -.

Receptor.
1 1
NON_TER 1
1 NON_TER 43 43
SEQUENCE 433 AA; 45723 MW; 75736D835E72CA4
                                                                                                                                                                                    neurotrophin receptor.";
                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; I
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea;
                                                                                                                                                                                                                                                                                                                                  Q9PRG7
                                             PROSITE;
                                                                                                                                                                                          "Life and death in
                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                NCBI_TaxID=8355
                                                                                                                                                                                                                                          Xenopodinae;
                                                                                                                                                                                                                                                                                                                                                                                              235
                                                                                                                                                                                                                                                                                                                                                                                                                203
                                                                                                                                                                                                                                                                                                                                                                                                                                  186
                                                                                                                                                                                                                                                                                                                                                                                                                                                    147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100
                                                                                                                                                                                                                                                                                                                                                                              259
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              42
Match
                                                                                                                                                                                                                                                                                                                                                   8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CCHECRPGNGMVSRCSRSQNTVCRPCGPGFYNDVVSSKPCKPCTWCNLRSGSERKQL--C
                                                                                                                                                                                                                                                                                                                                                                              LANCFILVORKKKP
                                                                                                                                                                                                                                                                                                                                                                                              LA-LYLLRRDQRLP
                                                                                                                                                                                                                                                                                                                                                                                                                PTRSQPMDQEPGPSQTPHIPVSLGSTPIIEPSITGGIS----LPIGLIVGLTTLGLLMLG
                                                                                                                                                                                                                                                                                                                                                                                                                                  PITVQPTEAWPRTSQGP-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                    APGTFSDTTSSTDVCRPHRICSILA----IPGNASTDAVCASESPTPSAVPRTIYVSQPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PPGHFS--PGDNQACKPWTNCTLAGKHTLQPASNSSDAICEDRDP-PATQPQETQGPPAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TKKQNRVCACNA-----DSYCALKLHSGNCRQCMKLSKCGPGFGVARSRTSNGNVICSAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TATQDTVCRCRAGTQPLDSY--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CCAKCPPGQYAKHFCNKTSDTVCADCAAGMFTQVWNH--LHTCLSCSSSCSDDQVETHNC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                           PS50017; DEATH_DOMAIN; 1.
PS01186; EGF_2; UNKNOWN_1.
PS00652; THER_NGER_1; UNKNOWN_3
PS50050; THER_NGER_2; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1
433
433
                           401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                     Richards A.P.,
                                                                                                                                                                                                                                        Xenopus.
                           ₹,
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433
45723 <sub>1</sub>
                                                                                                                                                                                             the
                                                                                                                                                                                                                                                                                                                                                                              272
                           43419 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13.4%;
26.8%;
13
                                                                                                                                                                                           developing
                                                                                                                                                                                                                                                                                      A-2.
                                                                                                                                                                                                                                                                                             Last sequence up
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               34;
                                                                                                                                                                         EMBL/GenBank/DDBJ
                                                                                                                                                                                                      Bothwell
                                                                                                                                                                                                                                                                                                               Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score
Pred.
Score
                                                                                                                                                                                                                                                                                                                                                                                                                                 STRPVE--VPGGRAVAAILGLGLVLGL--LGPLAIL
                                                                                                                                                                                                                                                                                                                                   PRT;
                           D13BCAF7863EFECF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          75736D835E72CA4A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                           Xenopus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      205.5;
No. 7.2
204
                                                                                                                                                                                                                                                                                                                                   401
5.
                                                                                                                                                                                                                                                         Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ----KPG----
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                                                                                                                                                                                           retina:
                                                                                                                                                                                                                                                                                                       update)
DΒ
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                                                                                                                                                                                                                                                                                              update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; 68
                                                                                                                                                                          databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       databases
13;
                           CRC64;
                                                                                                                                                                                            The
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Length
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                                                                                                                                                                                            of.
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                                                                                                                                                                                            the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      185
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Best Local
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                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                InterPro; IPR001368; TNFR_c6.
Pfam; PF00020; TNFR_c6; 3.
ProDom; PD000771; TNFF_C6; 1.
SMART; SM00208; TNFR; 3.
PROSITE; PS00652; TNFR_NGFR_1; 1
PROSITE; PS00652; TNFR_NGFR_2; 3
NON_TER 169 169
SEQUENCE 169 AA; 18525 MW; F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-OCT-2000 (TrEMBLrel. 15, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
CD40 PROTEIN (FRAGMENT).
Rattus norvegicus (Rat).
Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q9JKEO;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gao
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 62-169 FROM N.A.
STRAIN-WISTAR; TISSUE-SMOOTH MUSCLE, AORTA;
MEDLINE-99330195; PubMed-10403401;
KIZESZ R., Wagner A.H., Cattaruzza M., Hecker M.;
"Cytokine-inducible CD40 gene expression in vascular smooth muscle cells is mediated by nuclear factor kappaB and signal transducer ar activator of transcription-1.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (MAR-2001) to the EMBL; AF241231; AAF43717.2; HSSP; P25942; ICDF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEBS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=WISTAR; TI
Gao D., Hecker M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Krzesz R., Hecker M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-WISTAR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local
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                                                                                                                   26
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                                                                                                                      VTGLH----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lett. 453:191-196(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LRSGSERKQL-CTATQDTVCRCRAG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CVGDTYPSNDRCCHECRPGNGMVSRCSRSQNTVCRPCGPGF-YNDVVS-SKPCKPCTWCN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SSDFPYTGTSVPPFDLSSSSA---TTSGDSKVLPPTGVAENLIPVYCSILAAVIAGLV 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TQPQETQGPPARPITVQPTEAWPRTSQG-----PSTRPVE--VPGGRAVAAILGLGLV 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ---CEKCPEGTYSDEDNDRDPCLPCTICE-DGEIEAKECTFTSDTVCYDPNPRVSSVTPA 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GVDCAPCPPGHFSPGDN--QACKPWTNCTLAGKHTLQPASNSSDAICEDRDP-----PA 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   --FGHKRMEAPCVESDDAVCACAYGYFTDKKSGQCKLCKSCPEGFGMMMSCTNIQDTI-- 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CWSGQYTAKGECCISCQVGEGVIKRCGVNQ-TVCEPCLDSVTYSDTISHTEACKPCTEC- 79
                        - PCKPCTWCNLRSGSERKQLCTATQDTVCRCRAG
                                                                    LTAVHLGQCVTCSDKQYLQGGECCDLCQPGNRLVSHCTALEKTQCQPCDSGEFSAHWNRE
                                                                                                                                                                    46;
                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (MAR-2000) to the
                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=SMOOTH MUSCLE, AORTA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE=SMOOTH MUSCLE, AORTA;
                                                                                                  -CVGDTYPSNDRCCHECRPGNGMVSRCSRSQNTVCRPCGPGFYNDVVSSK 79
  -
::
                                                                                                                                                                                          13.2%;
29.1%;
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                                                                                                                                                                    19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL/GenBank/DDBJ
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28; Mismatches 87;
                                                                                                                                                               Score 203.5; DB 11
Pred. No. 4.1e-11;
9; Mismatches 52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Craniata; Vertebrata; I
Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                   F199D91EFA224A26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            B
                                                                                                                                                                                                              DB 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          databases
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                                                                                                                                                                                                                                                                                     CRC64;
                                                                                                                                                                  Indels
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                                                                                                                                                                                                         Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Euteleostomí;
; Murinae; Rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ----TQPLDSYKP 121
                                                                                                                                                                                                                 169;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           57;
                                                                                                                                                                  41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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ID 202327
ID 206
DT 011
DT 011
DT 011
DT 011
DT 011
DT 011
RRA POOR MULL
RRA POOR RT 11
LA POOR RT 12
RRA POOR RT 12
RRA POOR RT 14
RRA POOR RT 14
RRA POOR RT 15
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RRA POOR RT 16
RRA POOR RT 17
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δÃ
                                            DЪ
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Best Local 9
                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VARIANT
VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Receptor.
NON_TER
VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=95178848; PubMed=7873884; Powell E.E., Wicker L.S., Peterso "Allelic variation of the type 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mamm. Genome 5:726-727(1994).
EMBL; X76401; CAA53981.1; -.
HSSP; P19438; INCF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gene."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Amino acid variation in the tumor Necrosis linked to autoimmune diabetes in NOD mice."; Genomics 0:0-0(0).
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                                                                                        ARPITVQPTEAWPRTSQGPS-----TRPV---EVPGGRAVAAILGLGLVLGLLGPLAIL
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                                                                                                                                                                                     --PGDNQACKPWTNCTLAGKHTLQPASNSSDAICEDRDP----PAT----QPQETQGPP
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TNFR_NGFR_2;
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Last annotation update)
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Pred. No. 1.8e
34; Mismatches
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6C51D2CF1C4626DF CRC64;
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No. 1.8e-10;
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                                                            InterPro; IPR001005; Myb_DNA_bind.
InterPro; IPR001865; Ribosomal_S2.
InterPro; IPR001368; TNFR_c6.
Pfam; PF00020; TNFR c6. 4
                                                                                                                                                                                   "Regulation or ....";
alternative splicing.";
alternative splicing.";
Natl. Acad. Sci. U.S.A. 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CD40
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Submitted (PEB-2001) to the
EMBL; BC002794; AAH02794.1;
                        Prodom; PD000771; TNFR_c6; 1. SMART; SM00208; TNFR; 4.
                                                                                                                                                               EMBL; AJ401389; CAC29429.1; HSSP; P25942; 1CDF.
                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. WEDLING-21117110; PubMed-11172023; MEDLING-21117110; PubMed-11172023; Tone M., Tone Y., Fairchild P.J., Wy "Regulation of CD40 function by its"
                                                                                                                                                                                                                                                                                                                                                                        Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalla; Eutherla; Rodentia;
NCBI_TaxID=10090;
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01-JUN-2001 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
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Mammalia; Eutheria;
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MYB_1; UNKNOWN_1
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Primates;
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28.8%;
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Pred. No. 4.7e
L4; Mismatches
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Matches 48
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Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                       Prodom; PD000771; TNFR_C6; 1.

SMART; SM00208; TNFR; 4.

PROSITE; PS000537; MYB_1; UNKNOWN_1.

PROSITE; PS00962; RIBOSOMAL_S2_1; UNFR_NOSITE; PS00652; TNFR_NOFR_1; 1.

PROSITE: PS50050; TNFR_NOFR_2; 4.

SEQUENCE 234 AA; 25747 MW; 00DB11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        O99NE2; PRELIMINARY;
O99NE2;
01-JUN-2001 (TrEMBLrel. 1
01-JUN-2001 (TrEMBLrel. 1
01-DEC-2001 (TrEMBLrel. 1
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PROSITE;
PROSITE;
SEQUENCE
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Proc. Natl. Acad. Sci. U.S.A.
PROS. AJ401388; CAC29428.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-21117110; PubMed-11172023; MEDLINE-21117110; PubMed-11172023; Tone M., Tone Y., Fairchild P.J., Wykes M., Wegulation of CD40 function by its isoforms
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR001005; Myb_DNA_bind.
InterPro; IPR001865; Ribosomal_S2.
InterPro; IPR001368; TNFR_c6.
Pfam; PF00020; TNFR_c6; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HSSP; P25942; 1CDF
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135
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VTGLH-----CVGDTYPSNDRCCHECRPGNGMVSRCSRSQNTVCRPCGPGFYNDVVSSK
                                                                                                                                                                                                                                VTGLH-----CVGDTYPSNDRCCHECRPGNGMVSRCSRSQNTVCRPCGPGFYNDVVSSK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -PCKPCTWCNLRSGSERKQLCTATQDTVCRCRAG------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LTAVHLGQCVTCSDKQYLHDGQCCDLCQPGSRLTSHCTALEKTQCHPCDSGEFSAQWNRE
ATETTDTV-
                                        -TQPLDSYKPGVDCAPCPPGHFSPGDNQA-----CKPWTNCTLAGKHTLQPASNSSDAIC
                                                                                        IRCHQHRHCEPNQGLRVKKEGTAESDTVCTCKEGQHCTSKDCEACAQHTPCIPGFGVMEM
                                                                                                                                   -PCKPCTWCNLRSGSERKQLCTATQDTVCRCRAG------
                                                                                                                                                                                   LTAVHLGQCVTCSDKQYLHDGQCCDLCQPGSRLTSHCTALEKTQCHPCDSGEFSAQWNRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATETTDTV-----CHPCPVGFFS---NQSSLFEKCYPWTSCEDKNLEVLQKGTSQTNVIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -TQPLDSYKPGVDCAPCPPGHFSPGDNQA-----CKPWTNCTLAGKHTLQPASNSSDAIC
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                                                                                                                                                                                                                                                                                                 Similarity
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PS00652; TNFR_NGFR_1; 1.
PS50050; TNFR_NGFR_2; 4.
222 AA; 24499 MW; EE:
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                                                                                                                                                                                                                                                                              Conservative
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-CHPCPVGFFS---
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19,
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                                                                                                                                                                                                                                                                           Score 193.5;
Pred. No. 4.8e
23; Mismatches
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Pred. No. 4.5e-
23; Mismatches
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                              00DB1DD38347E325 CRC64;
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EE21E6C76FB42DEF CRC64;
NQSSLFEKCYPWTSCEDKNLEVLQKGTSQTNVIC
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No. 4.5e-10;
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ns generated
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14

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RESULT
Q9XSZ8
ID Q9XSZ8
AC Q9

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Best Local S
Matches 78
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                                                                                                                                                                                                                       Cercopithecus aethiops (Green monkey) (Grivet).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
Cercopithecinae; Cercopithecus.
NCBI_TaxID=9534;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q9XSZ8;
01-NOV-1999 (TrEMBLrel.
01-NOV-1999 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
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OSada N., Hida M., Kusuda J., Tanuma R., Iseki K., Hirai
Suzuki Y., Sugano S., Hashimoto K.;
"Isolation of full-length cDNA clones from macaque brain
libraries.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     UNNAMED PORTEIN PRODUCT.

Macaca fascicularis (Crab eating macaque) (Cynomolqus monkey).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;

Cercopithecinae; Macaca.
MEDLINE=99296730; PubMed=10366573;
Foster T.P., Chouljenko V.N., Kousoulas K.G.;
"Functional characterization of the HveA homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8zsx60
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SMART; SM00208; TNFR; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                               HVEAS.
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                                                                                                                       TISSUE-KIDNEY;
                                                                                                                                                       SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AWPRTSQGPSTR----PVEVPGGRAVAAILGLGLVLGLLGPLAILLALYLLRRDQRLPPDA
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EMBL; AF147720; AAD37381.1; -.
HSSP; O14763; 1D0G.
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LIICVKRRKSR 234
                        LALYLLRRDQR 245
                                                                           PQETQGPPARPITVQPTEAWPRTSQGPSTRPVEVPGGRAVAAIL-GLGLVLGLLGPLAIL
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Search completed: June 18, 2002, Job time: 135 sec 14:26:16

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Copyright (c) 1993 - 2000 Comp
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ALIGNMENTS

ACT-4 cell surface receptor protein.

21-NOV-1995 (first entry)

AAR74737;

AAR74737 standard; Protein; 277

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03-NOV-1994; Domain Cleavage-site Cleavage-site Homo Cell surface receptor; ACT-4; T-lymphocyte; T-cell; immune system. 11-MAY-1995. WO9512673-A. Modified-site Modified-site Peptide sapiens. 94WO-GB02415 /note= "g 160..162 /note= "s 146..148 /note= "signal peptide" 22..23 24..25 /note= "glycosylation site"
214..240 Location/Qualifiers /note= "signal cleavage site" "signal cleavage site" "transmembrane domain" "glycosylation site"

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RESULT
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                                                                                                                                                            Homo
                                                                                                                                                                                                                           ACT-4; specific binding partner; sbd; B cells; lymphocyte; GVHD; graft versus host disease; immune response; transplantation; autoimmune disease; inflammation; HIV; human immunodeficiency virus; HTLV; human T lymphocyte virus; inflammatory bowel disease;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACT-4-L-h-1 is a specific binding partner (sbp) to the ACT-4 receptor polypeptide (encoded by this sequence) on the surface of activated CD4 positive B cells. The sbp and its fragments are useful in pharmaceutical compositions to modify a patient's immune response as well as having application in the treatment of transplant rejection, graft versus host disease, autoimmune disease, inflammation, infectious agents, HTLV infected cells or HIV. Specifically the sbd can be used to treat inflammatory bowel disease. The sbd can also be used for screening for immunomodulatory agents able to recognise ACT-4 and for monitoring activated CD4 positive cells or inhibiting infection of CD4 positive cells.
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useful i
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                                                                                                 NTVCRPCGPGFYNDVVSSKPCKPCTWCNLRSGSERKOLCTATQDTVCRCRAGTQPLDSYK 120
                                                       RRDQRLPPDAHKPPGGGSFRTPIQEEQADAHSTLAKI
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18-AUG-1999;
20-AUG-1999;
10-SEP-1999;
                                                                                                                                                                                                                                                                                                                                      The present invention provides the protein and coding sequences of the human tumour necrosis factor receptors TRI3 and TRI4. These sequences useful in the diagnosis and treatment of many diseases, including cance autoimmune diseases, cardiovascular disorders, allergies,
                                                                                                                                                                                                                                                                                                                                                                                                                       Nucleic acids encoding 2 human tumor necrosis factor receptor polypeptides ((TR13)) and (TR14)), useful for the prevention, diagnosis and treatment of, e.g. cancers, acquired immune deficiency syndrome and hypohidrotic ectodermal dysplasia.
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                                                                                           pgvdcapcppghfspgdnqackpwtnctlagkhtlqpasnssdaicedrdppatqpqetq
                                                                                                                  PGVDCAPCPPGHFSPGDNQACKPWTNCTLAGKHTLQPASNSSDAICEDRDPPATQPQETQ
                                                                                                                                       ntvcrpcgpgfyndvvsskpckpctwcnlrsgserkqlctatqdtvcrcragtqpldsyk
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99US-0149450.
99US-0149712.
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Pred. No. 1.2e-100;
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The present invention describes the human TRID protein (tumour necrosis CC factor (TNF) related apoptosis inducing ligand (TRAII) receptor without CC intracellular domain, also referred to as tumour necrosis factor CC receptor 5 (TNF) also referred to as tumour necrosis factor CC entivities, and can be used in gene therapy. The TRID polynucleotides are useful for detecting complementary polynucleotides. TRID proteins and CC polynucleotides are useful in the treatment of tumours, resistance to CC parasite, bacteria and viruses, restenosis and graft versus host disease. CC and to prevent certain haematopoletic cells, to regulate antiviral responses CC and to prevent certain autoimmune diseases after stimulation of TRID by CC an agonist or TRAIL binding facilitator. The antibodies which bind TRID CC polynucleotides, proteins, antibodies, agonists and antagonists are cuseful for treating and/or preventing diseases (C cuseful in the diagnosis, treatment or prevention of: (a) cancer; CC useful in the diagnosis, treatment or prevention of: (a) cancer; CC is autoimmune discases associated with increased cor decreased associated with increased in CC comparison with TRID in the exemplification of the present invention. The present sequence represents a tumour necrosis factor receptor used in CC comparison with TRID in the exemplification of the present invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nucleic acid encoding a TRID polypeptide, also referred to necrosis factor receptor 5, useful in the diagnosis, treatm prevention of cancer, autoimmune disorders and viral infect
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RESULT
AAR76996
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         antigen activated T-cells, especially, for example, CD4+ T-cells. A C human cDNA encoding the human OX-40 homologue was cloned as follows. Using the Experimental Autoimmune Encephalomyelitis model in rats the OX-40 antigen was identified (expressed on the surface of activated autoantigen-specific CD4+ T-cells present at the site of inflammation but absent on CD4+ T-cells at non-inflammatory sites) and cDNA encoding the antigen was isolated. PCR primers were designed and used to clone murine OX-40 cDNA by PCR from RNA isolated from murine CD4+ T-cells activated with concanavalin A. Then the murine OX-40 cDNA was used to probe a cDNA lambda gtl1 library from human activated T lymphocytes to obtain human OX-40 cDNA the sequence is also in SQ ID no. 1, but this sequence is not present the number of the normal color of the received by it are claimed.
                                                                                                                                                                                                                                                                                                                                                                                                                                     Nucleic acid encoding an activated T-cell antigen, Ox-40 - used develop prods. for detection and therapy of conditions mediated activated T-cells, eg. multiple sclerosis, rheumatoid arthritis,
                                                                                                                                                                                                                                                                                                                                               Antigen OX-40 is specifically expressed on the cell surface of
                                                                                                                                                                                                                                                                                                                                                                                       Claim 3; Fig 11; 91pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1995-283771/37.
N-PSDB; AAQ93257.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Vandenbark AA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              06-FEB-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               T-cell lymphoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human Ox-40; activated T-cells; CD4+ T-cells; antigen;
multiple sclerosis; sarcoldosis; rheumatoid arthritis; uveitis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       multiple sclerosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Deduced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21-DEC-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (WEIN/) WEINBERG A D. (CANT-) CANTAB PHARM RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10-AUG-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo
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encoded
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Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                This plasmid encoues an converge mutein fusion protein for and is used to express a soluble OX40/FC mutein fusion protein for use in detecting cDNA clones encoding a OX40 ligand. The FC fragment may be derived from human IgG1, and the plasmid may be used to transform the CV-1/EBNA (ATCC CRL 10478) monkey kidney celline. Culture supernatant was purified by affinity chromatography time. Culture supernatant was purified by affinity chromatography
                                                                                                                                                            New isolated DNA encoding the OX40 ligand polypeptide and host cells, used to produce recombinant ligand used prim. T cell culture, to modulate immune response etc.
                                                                                                                                                                                                             WPI; 1995-357992/46.
N-PSDB; AAT00829.
Sequence
                                                                                                                                                                                                                                                 Baum
                                                                                                                                                                                                                                                                                                23-JUL-1993;
                                                                                                                                                                                                                                                                                                                        23-JUL-1993;
                                                                                                                                                                                                                                                                                                                                                                         US5457035-A
                                                                                                                                                                                                                                                                                                                                                                                                Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                       pDC406/OX40/Fc*;
                                                                                                                                                                                                                                                                                                                                                                                                                                    OX40; OX40-L;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Plasmid pDC406/OX40/Fc* encoding an OX40/Fc mutein protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30-MAR-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAR81882;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAR81882 standard;
                                                                                                                                    Example
                                                                                                                                                                                                                                                                     (IMMV ) IMMUNEX CORP
                                                                                                                                                                                                                                                                                                                                                10-OCT-1995
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                                                                                                                                                                                                                                                 PR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            plasmid encodes an OX40/Fc antibody fragment mutein protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RRDQRLPPDAHKPPGGGSFRTPIQEEQADAHSTLAK 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GPPARPITVQPTEAWPRTSQGPSTRPVEVPGGRAVAAILGLGLVLGLLGPLAILLALYLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             rrdqrlppdahkppgggsfrtpiqeeqadahstlvk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               269;
                       various
                                                                                                                                    2; Column 35-38;
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                                                                                                                                                                                                                                                 Fanslow WC,
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                        cell
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97.5%;
                                                                                                                                                                                                                                                 Gayle
                                                                                                                                   26pp; English.
                                                                                                                                                                                                                                                 RВ,
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Pred. No. 1
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                                                                                                                                                                                                                                                 Goodwin RG;
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L.1e-97;
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RESULT
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Chimeric
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OX40/Fc;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAW48976 standard;
                    Example
                                                   Purified polypeptide OX-40 ligands production and binding assays for C
                                                                                                                                                                 Baum
                                                                                                                                                                                                  (IMMV ) IMMUNEX CORP
                                                                                                                                                                                                                                      23-JUL-1993;
22-JUN-1995;
                                                                                                                                                                                                                                                                                           22-JUN-1995;
                                                                                                                                                                                                                                                                                                                                 21-JUL-1998
                                                                                                                                                                                                                                                                                                                                                                   US5783665-A.
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                                                                                                                                                               PR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1998-427099/36
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                    2;
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                                                                                                            AAV32636
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cytokine;
                                                                                                                                                               Fanslow WC,
                    Col
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo
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                    37-40;
                                                                                                                                                                                                                                    93US-0097827
95US-0494574
                                                                                                                                                                                                                                                                                             95US-0494574
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note=
225
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "Extracellular domain of mouse OX40"
207..438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                           /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      T cell antigen; TH-2 immune response;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             44.0%;
63.3%;
                   26pp; English
                                                                                                                                                                                                                                                                                                                                                                                                      "changed mutant"
                                                                                                                                                                                                                                                                                                                                                                                                                                                           "changed
mutant"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "changed mutant"
                                                                                                                                                               Gayle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Mutant Fc region of human IgG1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Score 676.5; DB; Pred. No. 7e-40; 17; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       438
                                                                                                                                                               RB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   from
                                                                                                                                                                                                                                                                                                                                                                                                                       from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              from
                                                     3 - for co:stimulation of T-cell
OX-40 and homologues
                                                                                                                                                               Goodwin
                                                                                                                                                                                                                                                                                                                                                                                                                       Gly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Leu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Leu in wild-type to Ala
                                                                                                                                                                                                                                                                                                                                                                                                                       in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              in
                                                                                                                                                               RG
                                                                                                                                                                                                                                                                                                                                                                                                                       wild-type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            wild-type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                         б
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       antibody"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OX40-L;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ω
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190

ttvwprtselpstptlvep

208

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                                                                                                                                                                                                                                                                Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                            The present sequence represents the OX40/Fc fusion protein that contains the extracellular domain of mouse OX40 fused to the mutated Fc region of the human IgGl antibody. The fusion protein was used for detecting cDNA clones encoding an OX40 ligand. The invention claims for a murine OX40-L cytokine (AAW48975) that binds to the murine T cell antigen, OX40. The OX40-L protein is claimed to be useful for co-stimulation of T-cell production and in binding assays for detecting OX40 or its homologues. The OX40-L protein is also claimed to generate a TH-2 immune response.
                                                                                                                                                                                                                                                                                                                                Sequence
               192
                                                130
                                                                                 132
                                                                                                                70
                                                                                                                                               74
                                                                                                                                                                               10
                                                                                                                                                                                                              15
TEAWPRTSQGPSTRPVEVP 210
                                                               HFSPGDNQACKPWTNCTLAGKHTLQPASNSSDAICEDRDPPATQPQETQGPPARPITVQP 191
                                                                                                                             allllgltlgvtarrlncvkhtypsghkccrecqpghgmvnrcdhtrdtlchpcetgfyn
                                                                                                            eavnydtckqctqcnhrsgselkqnctptqdtvcrcrpgtqprqdsgyklgvdcvpcppg
                                                                                                                                                                                                             ALLLLGLGLS-TVTGLHCVGDTYPSNDRCCHECRPGNGMVSRCSRSQNTVCRPCGPGFYN 73
                                              hfspgnngackpwtnctlsgkgtrhpasdsldavcedrsllatllwetgrptfrpttvqs
                                                                                                                                                                                                                                                 126;
                                                                                                                                                                                                                                             Similarity 63.3
26; Conservative
                                                                                                                                                                                                                                                                                                                                  438 AA;
                                                                                                                                                                                                                                                                44.0%;
63.3%;
                                                                                                                                                                                                                                               17;
                                                                                                                                                                                                                                               Score 676.5; DE Pred. No. 7e-40; 7; Mismatches
                                                                                                                                                                                                                                                                                DB 19;
                                                                                                                                                                                                                                                 53;
                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                            Length
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                                                                                                                                               131
                                                                                                                                                                               69
                                                189
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RESULT
AAB66985
                                                                                                                                                                                                                                                                                                                                  Bone loss; osteoprotegerin; OPG; rheumatoid arthritis; hyperalgesia; multiple sclerosis; osteoprorosis; osteomyelitis; asthma; inflammation; systemic lupus erythematosus; graft-versus-host disease; septic shock; acute pancreatitis; Alzheimer's disease; anorexia; atherosclerosis; pa coronary condition; myocardial infarction; cancer; diabetes; psoriasis ocronary condition; myocardial infarction; cancer; diabetes; psoriasis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0x40
                                                                                                              07-JUL-2000;
                                          09-JUL-1999;
09-DEC-1999;
                                                                                                                                                                                                     WO200103719-A2
                                                                                                                                                                                                                                                  Unidentified.
                                                                                                                                                                                                                                                                                                                    endometriosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAB66985;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAB66985
                                                                                                                                                         18-JAN-2001.
                                                                                                                                                                                                                                                                                               ischaemia;
(AMGE-) AMGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                œ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      standard;
                                                                                                                                                                                                                                                                                             sis; fever; glomerulonephritis;
Parkinson's disease.
                                                                                                                 2000WO-US18667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                          99US-0350670
99US-0457647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      205
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disease;

pain;

Treating conditions leading to bone loss such as rheumatoid arthritis, multiple sclerosis and asthma, comprises administering an

O

.g. inhibitors

ō,

Boyle WJ,

Lacey DL,

Calzone

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Chang ĭ

Senaldi

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2001-103031/11

osteoprotegerin protein in conjunction with interleukin and tumor necrosis factor alpha

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RESULT
AAR81881
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention relates to a method for treating conditions leading CC to bone loss. The method comprises administering a purified and isolated osteoprotegerin (OPG) protein (AAF57836-AAF57838 and AAB66974-AAB66976) CC in conjunction with other substances such as tumour necrosis factor-alpha CC (TNF-alpha) inhibitors, interleukin (II)-6, -8 and -18 inhibitors, ICE CC modulators, fibroblast growth factor (FGF)1-10 modulators and/or platelet CC activating factor (PAF) antagonists. The method is useful for treating CC conditions leading to bone loss such as rheumatoid arthritis, multiple CC sclerosis, osteoporosis, osteopyelitis and asthma. The method is also CC useful for treating inflammation, systemic lupus crythematosus (SLE) and graft-versus-host disease (GvHD). Other diseases that can be treated CC include acute pancreatitis, Alzheimer's disease, anorexia, CC annear, diabetes, endometriosis, fever, glomerulonephritis, hyperalgesia, CC inflammatory bowel disease, ischaemia, pain, Parkinson's disease, concared concertion and septic shock. The present sequence was used in a sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local
                                                                                                                                                                                                                                                           membrane
                        WPI; 1995-357992/46
                                                   Baum PR,
                                                                                                               23-JUL-1993;
                                                                                                                                            23-JUL-1993;
                                                                                                                                                                         10-OCT-1995
                                                                                                                                                                                                    US5457035-A
                                                                                                                                                                                                                               Mus musculus
                                                                                                                                                                                                                                                                           OX40; OX40-L;
                                                                                                                                                                                                                                                                                                     Mouse type-II membrane polypeptide OX40 extracellular domain.
                                                                                                                                                                                                                                                                                                                                  08-JUL-1996 (first entry)
                                                                                                                                                                                                                                                                                                                                                                 AAR81881;
                                                                                                                                                                                                                                                                                                                                                                                           AAR81881 standard; Protein; 206 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                  (IMMV ) IMMUNEX CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Fig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    190
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15 ALLLLGLGLSTVTGLHCVGDTYPSNDRCCHECRPGNGMVSRCSRSQNTVCRPCGPGFYND 74
5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                         9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EAWPRTSQGPST 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FSPGDNQACKPWTNCTLAGKHTLQPASNSSDAICEDRDPPATQPQETQGPPARPITVQPT 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 avnydtckqctqcnhrsgselkqnctptedtvcqcrpgtqprqdsshklgvdcvpcppgh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VVSSKPCKPCTWCNLRSGSERKQLCTATQDTVCRCRAGTQPL--DSYKPGVDCAPCPPGH 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           aflllglslgvtvklncvkdtypsghkccrecqpghgmvsrcdhtrdtvchpcepgfyne
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         fspgsnqackpwtnctlsgkqirhpasnsldtvcedrsllatllwetqrttfrpttvpst 189
                                                                                                                                                                                                                                                           glycoprotein.
                                                     Fanslow WC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             205 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                        cytokine;
                                                                                                               93US-0097827
                                                                                                                                            93US-0097827
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      <u>ب</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      316pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 44.08;
                                                     Gayle
                                                                                                                                                                                                                                                                          cell surface molecule
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 676;
Pred. No. 3
                                                     RВ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                     Goodwin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 22;
.5e-40;
                                                     RG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length
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                                                                                                                                                                                                                                                                                                                                                    RESULT 10
AAW48977
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SXX CCC X XX PT TXX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 43.9
Best Local Similarity 64.8
Matches 125; Conservative
                                                                                                 Baum
                                                                                                                                                                                                                                                                                                                                           AAW48977 standard; Protein; 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This sequence encodes the extracellular domain of OX40, a membrane glycoprotein present on the CD4 positive subset of activated T cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New isolated DNA encoding the OX40 ligand polypeptide - also we and host cells, used to produce recombinant ligand used in e.g. prim. T cell culture, to modulate immune response etc.
                  Example 1;
                                    Purified polypeptide OX-40 ligands - for production and binding assays for OX-40 \epsilon
                                                                     N-PSDB; AAV32640.
                                                                              WPI; 1998-427099/36.
                                                                                                                    (IMMV ) IMMUNEX CORP
                                                                                                                                        23-JUL-1993;
22-JUN-1995;
                                                                                                                                                                      22-JUN-1995;
                                                                                                                                                                                         21-JUL-1998
                                                                                                                                                                                                             US5783665-A
                                                                                                                                                                                                                                Mus sp.
                                                                                                                                                                                                                                                    OX40/Fc
                                                                                                                                                                                                                                                             OX40; cytokine; T cell antigen; TH-2 immune response; OX40-L;
                                                                                                                                                                                                                                                                                 Mouse 0X40 extracellular domain
                                                                                                                                                                                                                                                                                                     25-SEP-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; AAT00826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 1; Column 33-34; 26pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                   130
                                                                                                                                                                                                                                                                                                                                                                                                                192
                                                                                                                                                                                                                                                                                                                                                                                                                                                      132
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15 ALLLLGLGLS-TYTGLHCVGDTYPSNDRCCHECRPGNGMVSRCSRSQNTVCRPCGPGFYN 73
                                                                                                                                                                                                                                                                                                                                                                                                                                TEAWPRTSQGPST 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       eavnydtckqctqcnhrsgselkqnctptqdtvcrcrpgtqprqdsgyklgvdcvpcppg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               allllgltlgvtarrlncvkhtypsghkccrecqpghgmvnrcdhtrdtlchpcetgfyn
                                                                                                 Fanslow WC,
                  Col 33-34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        206
                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                        93US-0097827.
95US-0494574.
                                                                                                                                                                      95US-0494574
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               43.98;
                26pp; English.
                                                                                                 Gayle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 675.5; 1
Pred. No. 3.8e
16; Mismatches
                                                                                                 RB,
                                                                                                                                                                                                                                                                                                                                           ζ
                                                                                                 Goodwin
                                   co:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .8e-40;
                                                                                                 RG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 16;
                                     :stimulation homologues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length
                                                of T-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        also vectors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ω
••
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                69
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The present sequence represents the mouse OX40 extracellular domain

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RESULT 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Qγ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Qy
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Best L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The extracellular domain of OX40 is its ligand binding domain. The CDNA (AAV32640) encoding OX40 extracellular domain was used in the construction of the chimeric OX40/Fc CDNA (AAV32640). The invention claims for a murine OX40-L cytokine (AAW48975) that binds to the OX40 murine T cell antigen. The OX40-L protein is claimed to be useful for co-stimulation of T-cell production and in binding assays for detecting OX40 or its homologues. The OX40-L protein is also claimed to generate a TH-2 immune response.
                                                              New compounds designed from a binding loop of a tumour necrosis factor receptor - are capable of inhibiting the biological activities of tumour necrosis factor, e.g., in treating inflammor autoimmune diseases
                                                                                                                             WPI;
                                                                                                                                                                                                                                                                                                                                         Tumour necrosis factor receptor; TNF-R; autoimmune diseases; inflammation; septic shock; cachexia; graft versus host diseskin allergic reaction; immune complex disease; malaria;
                                       Disclosure;
                                                                                                                                                     Greene MI,
                                                                                                                                                                                                                                                      03-DEC-1998
                                                                                                                                                                                                                                                                               W09853842-A1
                                                                                                                                                                                                                                                                                                                                                                                            TNF-R extracellular Cys-rich domain OX40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAW94649 standard; peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
              The present
                                                                                                                                                                              (UYPE-)
                                                                                                                                                                                                      30-MAY-1997;
                                                                                                                                                                                                                             29-MAY-1998;
                                                                                                                                                                                                                                                                                                       Homo
                                                                                                                                                                                                                                                                                                                                transplantation
                                                                                                                                                                                                                                                                                                                                                                                                                      29-APR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                               AAW94649
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   eavnydtckqctqcnhrsgselkqnctptqdtvcrcrpgtqprqdsgyklgvdcvpcppg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hfspgnngackpwtnctlsgkgtrhpasdsldavcedrsllatllwetgrptfrpttvgs 189
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                                                                                                                                                    Murali R,
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              invention
                                      Fig 1; 78pp;
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                                                                                                                                                                              PENNSYLVANIA.
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                                                                                                                                                                                                                             98WO-US10891
                                                                                                                                                                                                                                                                                                                                rejection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    43.9%;
describes peptides and peptide analogues sequence to a binding loop of a tumour no
                                                                                                                                                     Takasaki
                                      English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16;
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Pred. No. 3.8e
16; Mismatches
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              which
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a tumour necrosis

osteoclastogenesis and bone resorption. Osteoclastogenesis and bone resorption inhibiting peptide analogues from the present invention have osteopathic, cytostatic, antirheumatic, antiarthritic, antiinflammatory

and are

factor (TNF) -

immunomodulatory activities,

The present invention describes a method for inhibiting

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Вb
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Best Local S
Matches 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         responses, septic shock, cachexia, autoimmunity, graft-versus-host disease, skin allergic reactions, immune complex disease, transplantation rejection and malaria. Administration is, e.g. oral transdermal, transmucosal, pulmonary, subcutaneous, intravenous or intramuscular. Parenteral dosage is 0.1-5 mg/kg/day. The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 factor receptor (TNF-R) superfamily member. The compounds are est designed from a binding loop of TNF-R p55. They are capable of inhibiting TNF binding to its cellular receptors and may be used inhibit the biological activities of TNF. They may be used in triple the biological activities of TNF. They may be used in triple the second conditions such as acute and chronic inflammatory the second conditions such as acute and chronic inflammatory.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Paget's disease; metastatic bone disease; rheumatoid arthritis; periodontal disease; modulating dendritic cell maturation; T cell proliferation. TONAL TOWNSTAND TO TOWNSTAND TOWNSTAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         osteoclastogenesis; bone loss; bone resorption; osteopathic; cytost antirheumatic; antiarthritic; antiinflammatory; immunomodulatory; tumour necrosis factor-related activation-induced cytokine; TRANCE; receptor activator of NF-kappaB ligand; RANK; osteoporosis;
                                                                                                                                                                                                                                                      (UYPE-)
                                                                                                                                                                                                                                                                                                28-JUL-1999;
                                                                                                                                                                                                                                                                                                                            28-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                         08-FEB-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human TNF-R extracellular Cys-rich domain OX40 SEQ ID NO:10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30-APR-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sequence represents an extracellular Cys-rich
                                                                                                                                                                                                                          (BARO/)
                                                                                                                                                                                                                                       (HORN/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cell
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                                                                                                               of peptides and peptide analogs which are {\tt TRANCE/RANK} inhibitors, inhibiting osteoclastogenesis and bone resorption -
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                                                                                                                                                               2001-182866/18.
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56; Conser
                                                                                                                                                                                                                                                                 UNIV PENNSYLVANIA
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                                                                                                                                                                                           Horne WC,
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llarity 100.0%;
Conservative
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                                                                                   81pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                               CD40 receptor
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Pred. No.
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2.2e-16;
                                                                                                                                                                                             Murali
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The compounds are especially
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               domain of TNF-R from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      osteopathic; cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       osteoclast;
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Best Local S
Matches 56
The present invention describes the human TRID protein (tumour necrosis factor (TNF) related apoptosis inducing ligand (TRAIL) receptor without intracellular domain, also referred to as tumour necrosis factor receptor 5 (TNFR-5 or TRS)). TRID has cytostatic, immunosuppressive, nootropic, neuroprotective, antiviral, antiinflammatory, anticonvulsant, antivitaes, and can be used in gene therapy. The TRID polynucleotides are useful for detecting complementary polynucleotides. TRID proteins an polynucleotides are useful in the treatment of tumours, resistance to parasite, bacteria and viruses, restenosis and graft versus host disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; tumour necrosis factor receptor 5; TRID; TNFR-5; TRS; nootropic TRAIL receptor without intracellular domain; diagnosis; cytostatic; tumour necrosis factor related apoptosis inducing ligand; vasotropic; immunosuppressive; neuroprotective; antiviral; antiinflammatory; anticonvulsant; antiparasitic; cardiant; anti-HTV; antiparkinsonian; gene therapy; restenosis; graft versus host disease; tumour; cancer; apoptotic cell death related disease; autoimmune disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              disease, and modulating dendritic cell maturation, T cell proliferation, and/or CD40 receptor systems. The present sequence represents an extracellular Cys-rich domain of a tumour necrosis factor receptor (TNF-R) superfamily member, which is used in the exemplification of the present invention.
                                                                                                                                                                                                                  related activation induced cytokine (TRANCE)/ receptor activator of NF-kappaB ligand (RANK) inhibitors. The method is useful for treating diseases characterised by bone loss such as osteoporosis, Paget's disease, metastatic bone disease, rheumatoid arthritis or periodontal
                                                                                                                                                                                       Disclosure; Fig 2;
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                                                                                                                                                                                                                                                                                                                                                                                        20-MAY-1999;
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                                                                                                                                                                                                                                                                                                                       Ruben
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                                                                                                                                                                                                                                                                                                                                                                                                                                       RANK
                                                                                                                                                                                                                                                                                                                                                RANK; necrosis factor-kappa B; NF-kB; receptor activator; immune response; inflammatory response; toxic shock; seps
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                                                                                 22-DEC-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                    polypeptide partial sequence encoded by cDNA clone 9D-15C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            aecrcqpgmscvyldnecvhceeerlvlcqpgteaevtdeimdtdvncvpckpghfqnts 181
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Best Local
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                  RANK; necrosis factor-kappa B; NF-kB; receptor activator; human; immune response; inflammatory response; toxic shock; sepsis; RANKL; RANK ligand; tumour necrosis factor; TNF.
                                                                                                                                        08-OCT-1998
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                                                                                              RANK polypeptide partial sequence encoded by cDNA clone 9D-15C.
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                                                                                                                                                                                                                                                                                                                                                LAGKHTLQPASNSSDAICEDRDPPATQPQE 178
                                                                                                                                                                                                                                                                                                                                                                                                                            --TQDTVCRCRAGTQ-----PLDSYKPGVDCAPCPPGHFSP--GDNQACKPWTNCT 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RCSRSQNTVCRPCGPGFYNDVVSSK-PCKPCTWCNL-----RSGSERKQLCTA-+
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70; Conservative
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33.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 247; DB 19;
Pred. No. 1.1e-09;
Pred. Mismatches 83;
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23-DEC-1996;
07-MAR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This represents a partial sequence of the polypeptide RANK (receptor activator of necrosis factor-kappaB (NF-kB)). RANK is a member of the tumour necrosis factor family. Host cells transformed or transfected with an expression vector comprising the RANK encoding nucleic acid can be used to produce recombinant RANK protein. The soluble RANK may be used for inhibiting activation of NF-kB, by contacting a cell expressing membrane-associated RANK with a soluble RANK which binds to RANK ligand (RANKL). The soluble RANK polypeptide composition may also be used for regulating an immune or inflammatory response. Inhibition of NF-kB by RANK antagonists may be useful in ameliorating negative effects of an
                                                                                                                                                                                                                                                                                                                                                                                                                             (RANKL). The soluble RANK polypeptide composition may also be used for regulating an immune or inflammatory response. Inhibition of NF-kB by RANK antagonists may be useful in ameliorating negative effects of an inflammatory response that result from triggering of RANK, e.g. in treating toxic shock or sepsis, graft-versus-host reactions, or acute inflammatory reactions. They can also be used in adjunct therapy for disease characterised by neoplastic cells that express RANK. The products can also be used for detection and drug screening.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New isolated receptor activator of necrosis factor-kappa for, e.g. developing products for regulating an immune on inflammatory response, treating toxic shock or sepsis
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                                                                                                                                                                                                                                                                1 MCVGARRLGRGPCAALLLL-----GLGLSTVTGLHCVGDT-YPSNDRCCHECRPGNGMVS 54
                                 LAGKHTLQPASNSSDAICEDRDPPATQPQE 178
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                                                                                                           --TODTVCRCRAGTO-----PLDSYKPGVDCAPCPPGHFSP--GDNQACKPWTNCT 148
                                                                                                                                                                                      RCSRSQNTVCRPCGPGFYNDVVSSK-PCKPCTWCNL------RSGSERKQLCTA-- 101
flgkrvehhgteksdavcssslparkppne
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97US-0813509.
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                                                                                                                                                                                                                                                                                                                     Score 247; DB 19; pred. No. 1.1e-09;
                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                          DB 19;
                                                                                                                                                                                                                                                                                                       83;
                                                                                                                                                                                                                                                                                                                                      Length 451;
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BG
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length: 2000000000
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Gapop 10.0 , Gapext 1.0
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ALIGNMENTS

RESULT 1.

AR048669
LOCUS
AR048669
AR0486691
VERSION
AR048669.1 GI:5971012
KEYWORDS
SOURCE
ORGANISM
Unknown.
ORGANISM
Unclassified.
TITLE
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176 a 390 c 344 g 147 t

Result No.

Score

Query Match Length

DB ID

Description

Query Match
Best Local Similarity

98.7%; 99.8%;

Score 1044.4; DB 6; Pred. No. 1.1e-150;

Length 1057;

Matches

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Unclassified.

1 (bases 1 to 1057).

1 (bases 1 to 1057).

Godfrey,W. and Engleman,E.G.

Godfrey,W. to a recepto:

T-cells

Patent: US 6242566-A 1 05-JUN
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Location/Qualifiers
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//Bi_xref="GI:913406"
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gaggctgccccccgatgcccacaagccccctgggggaggcagtttccggacccccatcca
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                                          ACGACCGGTGCTGCCACGAGTGCAGGCCAGGCAACGGGATGGTGAGCCGCTGCAGCCGCT
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X75962
X75962.1 GI:472957
OX40 antigen.
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Latza, U., Durkop, H., Schnittger, S., Ringeling, J., El Hummel, M., Fonatsch, C. and Stein, H.

The human OX40 homolog: cDNA structure, expression assignment of the AC735 antigen
assignment of the AC735 antigen
Bur. J. Immunol. 24 (3), 677-683 (1994)
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Location/Qualifiers
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90. .836
/product="OX40 |
814. .958
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/product="0X40 homologue"
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/protein_id="CAA53576.1"
/db_xref="G1:472958"
/db_xref="SWISS-PROT:P43489"
/db_xref="SWISS-PROT:P43489"
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ODTVCRCRAGTQPLDSYKPGYUCAPCPFGHFSPGDNQACKPWTNCTLAGKHTLOPASN
SSDAICEDRDPPATQPQETQGPPARPITVQPTEAWPRTSQGPSTRPVEVPFGGRAVAAI
LGLGLVLGLLGPLAILLALYLLRRDQRLPPDAHKPPGGGSFRTPIQEEQADAHSTLAK
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/db_xref="taxon:9606"
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AB003911

N Rabbit mRNA for OX40 precursor, partial cds.

AB003911 GI:2114107

OX40.

Oryctolagus cuniculus (sub_species:domesticus, stier)

HTV-I-transformed T cell_line:H446 cDNA to if the continuous continu
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                                                               2 (sites)
Isono,T. ar
                                                                                                                                     Direct Submission
Submitted (14-MAY-1997) Takahiro Isono, Shiga University of Medical Science, Central Research Laboratory; Seta Tsukinowachou, Otsu, Shiga 520-2192, Japan (E-mail:isono@belle.shiga-med.ac.jp, Tel:81-775-48-2308, Fax:81-775-48-2048)
Expression of OX40 HTLV-I-transformed
                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctola; 1 (bases 1 to 877)
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and OX40 ligand
T cell lines
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/cell_line="H446"
/cell_type="HTLV-I-transformed
<1...54
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/protein_id="BAA20059.1"
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/strain="Chbb:HM"
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                                                                                                                                                                                                                                                                                                                                                                      Chemistry: Dye-terminator ET-amersham; 16% of reads Chemistry: Dye-terminator Big Dye; 83% of reads Consensus quality: 110490 bases at least Q40 Consensus quality: 110677 bases at least Q30 Consensus quality: 110755 bases at least Q20 Insert size: 110819; sum-of-contigs Insert size: 160089; 6.7% error; agarose-fp Quality coverage: 8.36x in Q20 bases; sum-of-contigs Quality coverage: 8.95x in Q20 bases; agarose-fp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Direct Submission
Submitted (07-FEB-2002) Wellcome Trust Sanger Institute, Hinxton. Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Feb 10, 2002 this sequence version replaced gi:18642353.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens chromosome 1 clone RP5-902P8, PROGRESS ***, 4 unordered piecon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Assembly program: XGAP4; version 4.5 Sequencing vector: plasmid; L08752; 100% of reads
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Web site: http://www.sanger.ac.uk
Contact: humquery@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Center: Wellcome Trust Sanger Institute
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Mammalia; Eutheria;
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                                                                                                                                                                   NOTE: This is a 'working draft' sequence. It currently consists of 4 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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           42986 43085: gap of 100 bp

43086 54937: contig of 11852 bp

54938 55037: gap of 100 bp

55038 67254: contig of 12217 bp

67255 67354: gap of 100 bp

67355 111119: contig of 43765 bp
Location/Qualifiers
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ASE1; HTGS_ACTIVEFIN;
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Primates;
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caggigcaggccgcctgccccgccacgctcctgggccaactctgcaccgttctaggtgcc
                    | Ccaaggtggacgctgggccccgccaggctggagcccggagggtctgctgctgggcgagcaggg
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                                                                                                                                                                                                              gggcccctggccatcctgctggccctgtacctgctccggagggaccagaggctgcccc
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/clone_lib="RPCI-5"
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76.2%;
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Pred. No. 4.5e-51;
0; Mismatches 2;
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Homo sapiens chromosome 1 clone RP11-465B22,
PROGRESS ***, 29 unordered pieces.
AL390719
AL390719.25 GI:18476612
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (24-JAN-2002) Wellcome Trust Sanger Institute, Hinxton Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery&sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                  * NOTE: This is a 'working draft' sequence. It current
* consists of 29 contigs. The true order of the pieces
* is not known and their order in this sequence record
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: humquery@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            On Feb 1, 2002 this sequence version replaced
                                                                                                                                                                                                                                                                          * arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* record will be updated with the finished sequence
* This record will be updated with the accession number wil
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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be preserved.
8088: contig of 8088 bp in length
8089 8188: gap of 100 bp
8189 23213: contig of 15025 bp in length
23214 23313: gap of 100 bp
23214 23313: gap of 100 bp
23214 23720: contig of 3907 bp in length
23212 37320: gap of 100 bp
27221 27320: gap of 100 bp
30327 30426: gap of 100 bp
43167 43266: gap of 12740 bp in length
43167 43266: gap of 100 bp
47516: contig of 4250 bp in length
47516: gap of 100 bp
47517 47516: gap of 100 bp
47517 47516: contig of 4750 bp in length
47517 51392: contig of 3776 bp in length
51393 51492: gap of 100 bp
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47617. .51392
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197762: contig of 10544 bp in length
37862: gap of 100 bp
203431: contig of 5569 bp in length
3531: gap of 100 bp
206665.
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206862: contig of 3331 bp
06962: gap of 100 bp
210944: contig of 3982 bp
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/82 bp in length.
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447 accaactgcaccttggctgggaagcacaccctgcagccggccagcaatagctcggacgca 506

Query Match 36.8%; Best Local Similarity 76.2%; Matches 609; Conservative

Score 389.8; DB 2; Pred. No. 3.8e-51; 0; Mismatches 2;

Length 210944; Indels 188; Gaps

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BASE COUNT 38968 ORIGIN	misc_feature	misc_feature	misc_feature		misc_feature	CTECACAT	miso feature	misc_feature		misc_feature		misc_feature	######################################	mico foaturo	######################################	f 0 p + 11 r	mrsc_reacure	1	misc_reacure	h h	misc_reacure		misc_feature	,	misc_ieacure) h	misc_reacure	misc_feature		misc_feature		misc_feature		misc_feature	mitsc_tearnie	ħ	misc_feature
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assignment of the ACT35 antigen AL Eur J. Immunol. 24 (3), 677-683 (1994) NE 94170844	Hummel, M., Fonatsch, C. and Stein, H. The human OX40 homolog: cDNA structure. e	Eutheria; Coronaca; Cranidia; Veriebraca; Eutereos Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 to 5150)	e; rat OX40 antigen homologue.	ON Homo sapiens ox40 gene for CD134 an N AJ277151 GI:8926701	HSA277151 5150 bp DNA linear	Qy 1040 acaataaaaaccttggcag 1058	Db 9310 GATGGCTGCCTCCGGCTCTGCTTACGTATGCCATGCATACCTCCTGCCCCGGGGACC 9369	920 caggtgcaggcctgccccgccacgctcctgggccaactctgcaccgttctaggtgcc 9	Qy 860 ccaaggtggacgctgggccccgccaggctggagcccggagggtctgctgctgggcgagcaggg 919	Qy 800 catccaagaggagcaggccgacgccactccaccctggccaagatctgaccttgggccca 859	Qy 777 799 IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	Oy 758 cgatgcccacaagccccct	Qy 698 gggccccctggccatcctgctggccctgtacctgctccggagggaccagaggctgcccc 757	648googtgogttgocgcatoctgggcotggtgotggtgotggtct	Qy 648 647 647 Db 8831 CGAATAGGAGAAGGGGAGGGCGCATGGGGGCCCCTCCTGTGGACCCCACCCA	Qy 627 cggcccgtggaggtccccgggg	Qy 567 aggcccatcactgtccagcccactgaagcctggcccagaacctcacagggaccctccacc 626	Db 8591 AACAGCTTGCACCTTGGCAAGCACACCCTGCAGCCAGCAATAGCTCGGACGCA 8650 Qy 507 atctgtgaggaccagggaccccaggccacgcacgcaggagacccagggccccagggcc 566	0. COURT TO THE CO
	Š	/gene='0x40' /number=5 intron 3481. 3589	/gene="ox40" /number=4 284. 3480	/gene="0x40" /number="4 intron 27843283	intron 24302716 /gene="ox40" /number=3 exon 27172783	/number=2 23282429 /gene="ox40" /number=3	/gene="0x40" /number=2 intron 17582327 /gene="0x40"	intron 14381634 /gene="ox40" /number=1 exon 16351757	QDTVCRCRAGTQPLDSYKPGVDCAPCPPGHFSPGDNQACKPWTNCTLAGKHTLQPASN SSDATCEDRDPPATDPQETQGPPARPTTVQPTEAWPRTSQGPSTRPVEVPGGRAVAA1 LGLGLVLGLLGPLAILLALYLLRRDQRLPPDAHKPPGGGSFRTPIQEEQADAHSTLAK	/PIOGRO CAIS antigen /protein_id-"CAB96543.1" /db_xref="GI:8926702" /translation="McYGARRLGRGPCAALLLLGLGLSTVTGLHCVGDTYPSNDRCCH FCRBGNGMVXPGTSBONTVCRBDCBVNNVVSKDOKPCTWGNI.BRGSERKOICTAT	/gene="ox40" /note="rat Ox40 antigen homologue" /codon_start=1	/gene="ox40" /number=1 505 501 1293 . 1437,1635 . 1757,23282429,27172783, 32843480,35903718,37973867)	'UTR	mRNA join(1267. 1437.1635. 1757,23282429,27172783, 32843480,35903718,37974096) /geneox40" gene 12674096	urce	JOURNAL Submitted (28-MAR-2000) Pankow R., Inst. of Immunology, FU Berlin, University Hospital Benjamin Franklin, Hindenburgdamm 30, 12200 Berlin, GERMANY Berline SCHORENCE X75962.	NE 20318724 CE 3 (bases 1 to 5150) RS Pankow,R.	E 2 (bases 1 to 5150) S Pankow,R., Durkop,H., and Bulfone-Paus,S. The HTLV-I tax protei	

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Submitted (27-0CT-1989) Barclay A. N., MRC Cellular Immu
Unit, Sir William Dunn School of Pathology, South Parks:
Oxford OX1 3RE, U.K
2 (bases 1 to 1017)
Mallett, S., Fossum, S. and Barclay, A. N.
Characterization of the MRC OX40 antigen of activated CD
T lymphocytes--a molecule related to nerve growth factor
EMBO J. 9 (4), 1063-1068 (1990)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (11-FEB-1993) David M Calderhead, Molecular Immunology, Bristol-Myers Squibb, Pharmaceutical Research Institute, 3005 First Ave., Seattle, WA, 98121, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Calderhead,D.M., Buhlmann,J.E., van den Eertwegh,A.J., Claassen,E. Noelle,R.J. and Fell,H.P.
Clonding of mouse Ox40: a T cell activation marker that may mediate T-B cell interactions
J. Immunol. 151 (10), 5261-5271 (1993)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Mus musculus"
/strain="Balb/c"
/db_xref="taxon:10090"
/clone="pUCOx40.RJ.1"
/cell_line="TH2 D.10"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /protein_id="CAA79772.1"
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DAVCEDRSLLATLLWETQRPTFRPTTVQSTTVWPRTSELPSPPTLVTPEGPAFAVLLG
LGLGLLAPLTVLLALYLLRKAWRLPNTPKPCWGNSFRTPIQEEHTDAHFTLAKI"
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                               gagtgcaggccaggcaacgggatggtgagccgctgcagccgctcccagaacacggtgtgc
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Sequence 10
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AR019521.1
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Baum, P.R., Fanslow, W.C. III, Gayle, R.B.
Cytokine which is a ligand for OX40
Patent: US 5783665-A 10 21-UUL-1998;
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Unclassified.
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Pred. No. 8.5e-35;
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 CATCCGTGTGAGACTGGCTTCTACAATGAAGCTGTCAATTATGATACCTGCAAGCAGTGT
            cgtccgtgcgggccgggcttctacaacgacgtggtcagctccaagccgtgcaagccctgc
                                         GAGTGCCAGGCCATGGTATGGTGAACCGCTGTGATCATACCAGGGATACTCTATGT
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Sequence
114936
114936.1
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Baum, P.R., Fanslow, W.C. III, Gayle, R.B. and Cytokine which is a ligand for OX40

Patent: US 5457035-A 10 10-OCT-1995;
Location/Qualifiers
1. .1317
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417 c 337 g
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Pred. No. 8.5e-35;
0; Mismatches 209;
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                                                                                            ACACAGTGCAACCATCGAAGTGGAAGTGAACTCAAGCAGAATTGCACACCTACTCAGGAT
         acgtggtgtaacctcagaagtgggagtgagcggaagcagctgtgcacggccacacaggac
                                                             GAGTGCCAGGCCATGGTATGGTGAACCGCTGTGATCATACCAGGGATACTCTATGT
                                                                      gagtgcaggccaggcaacgggatggtgagccgctgcagccgctcccagaacacggtgtgc
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Sequence 6
AR019518
AR019518.1
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Baum, P.R., Fanslow, W.C. III, Gayle, R.B.
Cytokine which is a ligand for OX40
Patent: US 5783665-A 6 21-JUL-1998;
Location/Qualifiers
1. 618
                                                                                                                                                                                                                                    Unknown.
Unclassified.
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                                                                                                                                  Similarity
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Pred. No. 3.4e
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RESULT 14
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Sequence 6
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Baum, P.R., Fanslow, W.C. III, Gayle, R.B.

Cytokine which is a ligand for OX40

Patent: US 5457035-A 6 10-OCT-1995;

Location/Qualifiers
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                                                                                                                                  Similarity 70.0
94; Conservative
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5457035.
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3.4e-34;
nes 158;
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RESULT 15
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Search completed: June 18, Job time: 14967 sec
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Best Local Similarity 74.8%;
Matches 169; Conservative
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Patent: WO 0168912-A 304 20-SEP-2001;
Epigenomics AG (DE)
Location/Qualifiers
1. 6080
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Sequence 304 from Patent W00168912.
AX251336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          artificial sequence.

1 (bases 1 to 6080)

Olek,A., Piepenbrock,C. and Berlin,K.

Diagnosis of diseases associated with tumor suppressor genes and
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                                                                                                                                                                                                                                                                                                                                                                      /organism="synthetic construct"
/db_xref="taxon:32630"
/note="chemically treated genomic DNA (Homo sapiens)"
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 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Compugen Ltd
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BF063899 7h90a10.x
BI911081 603069733
BE349098 ht509055.x
AA991307 wu42d05.x
AA991207 wu42d05.x
AA9970291 0p09h05.x
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AA9306055 EST177040
AA501118 vf97h05.r
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5.7	5.7	5.7	5.7	5.7	5.7	5.7	5. 8	5.8	6.0	6.0	6.0	6.1	6.1	6.1	6.1	6.2	6.5	6.7	7.1	7.1	7.7	8.1	8.7	12.3	12.3	12.8	13.1
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                                                                                                                       source
                                                                                                                                  Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
Tissue Procurement: Ilan Kirsch, M.D., Michael R., Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         willd02.x1 NCI_CGAP_Co16 Homo sapiens cDNA clone ImAGE:2389923 3' similar to SW:OX40_HUMAN P43489 OX40L RECEPTOR PRECURSOR ;contains MER22.t3 MSR1 repetitive element ;, mRNA sequence.
AI738634
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Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 844)
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National Cancer Institute, Cancer Genome Anat
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/db_xref="taxon:9606"
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/clone_lib="NCI_CGAP_Co16"
                /tissue_type="colon tumor,
/lab_host="DH10B"
'note="Organ: colon; Vector: pT7T3D-Pac (Pharmacia) with
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603088095F1 NIH_MGC_120
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Subtraction by Bento Soares and M. Fatima Bonaldo. "
a 245 c 302 g 154 t 4 others
                 GI:15944991
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ccctgggggaggcagtttccggacccccatccaagaggagcaggccgacgcccactccac
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                                                       CCTGCTGGCCCTGTACCTGCTCCGGAGGGACCAGAGGCTG-CCCCCGATGCCACAAGCCC
                                                                        cctgctggccctgtacctgctccggagggaccagaggctgcccccgatgcccacaagcc
                                                                                                                               TGCGGTTGCCGCCATCCTGGGCCTGGGCCTGGTGCTGGGGCCTGCTGGGCCCCCTGGCCAT
                                                                                                                                              tgcggttgccgccatcctgggcctggggcctggtggggctgctggggccccctgggccat
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Clone distribution: MGC clone distribution information
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
plate: LLAM11571 row: m column: 24
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium
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National Institutes of Health, Mammalian
Unpublished (1999)
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/db_xref="taxon:9606"
/clone="IMAGE:5227199"
/clone_Iib="NHH_MGC_120"
/lab_host="DH10B"
/lab_host="DH10B"
/note="Organ: pooled pancreas and spleen; Vector:
pCMV-SpORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA
source anonymous pool of spleen and pancreas from 28 yo
male. Library is oligo-dT primed and directionally cloned
(EcoRV site is destroyed upon cloning). Average insert
size 1.5 kb, insert size range 1-2.5 kb. Library is
normalized and enriched for full-length clones and was
constructed by C. Gruber (Invitrogen). Research Genetics
tracking code 025. Note: this is a NIH_MGC Library."
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naff2a07.x1 Soares_NPBMC F
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MER22.tl TAR1 repetitive e
BG236062
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High quality sequence stop: 478.
Location/Qualifiers
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Mammalia; Eutheria;
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EST.
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National Cancer Institute, Cancer Genome Ana
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                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4141716"
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   Score 540; DB 10;
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element;, mRNA sequence.
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1 (bases 1 to 544)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Proje
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Ilan Kirsch, M.D., Michael R. Emme
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                                                           cDNA Library Preparation: M. Bento Soares, Ph.D. cDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Clone distribution: NCI-CGAP clone distribution information found through the I.M.A.G.E. Consortium/LLNL, send email to:
                               info@image.llnl.gov
Seg primer: -40UP from Gibco
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                                                                                                      BI911081 893
603069733F1 NIH_MGC_118 Homo
                                                                                mRNA sequence.
BI911081
  Mammalia;
              Eukaryota;
                           Homo sapiens
                                        human.
                                                                  в1911081.1
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38; Conservative
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//Organism="Homo sapiens"
//db_xerf="taxon:9606"
//dlone="IMAGE:332326"
//clone="IMAGE:332326"
//clone="IMAGE:332326"
//clone="Ib="NCI_GGAP_Col6"
//tissue_type="colon tumor, RER+"
//tissue_type="colon; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Plasmid DNA from the normalized library NCI_GRAP_Col0 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDs 1057416-1061255, and 1144584-1145351).
Subtraction by Bento Soares and M. Fatima Bonaldo. "
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; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                        sapiens cDNA clone IMAGE:5218473
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                                                                ctcagaagtgggagtgagcggaagcagtgtgcacggccacacaggacacagtctgccgc
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              CTTGGCTGGGAAGGCACACCCTGCAGCCGGCCAGCAATAGCTCGGACGCAATCTGTGAGG
                                                                                                                                                                                                                           GGGCTTCTACAAGCGACGTGGTCAGCTCCAAGCCTGTGCAAGCCCTGCACGTGGTGTAAC
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47.18; 92.98;

0;

Score 498.4; DB Pred. No. 1e-77; O; Mismatches

DB 10; 36;

Indels Length

13;

Gaps

11;

457

375 397

435

495

315

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REFERENCE
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JOURNAL
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plate: LLAM11549 row: b column: 10
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High quality sequence stop: 593.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies,
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National Institutes of Health, Ma
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
/note="Vector: pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA source leukocytes from anonymous pool of non-activated adult donors. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.7 kb, insert size range 1.2-3.3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 027. Note: this is a NIH_MGC Library."
                                                                                                                                                                                                                                                          /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="iMAGE:5218473"
/clone_lib="NIH_MGC_118"
/tisue_type="leukocyte"
/lab_host="bH108"
/note="Vector: pCMV-SPORT6: S
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cagggaccctccacccggcccgtggaggtccccggggggccgtgcggttgccgccatcctg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Chris Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D. cDNA Library Preparation: Life
Technologies, Inc. cDNA Library Arrayed by: Christa Prange,
I.M.A.G.E. Consortium DNA Sequencing by: Washington Univers:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Genome Sequencing Center Clone distribution information Clone distribution: NCI-CGAP clone distribution information found through the I.M.A.G.E. Consortium/LLNL, send email to:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BE34998 512 bp mRNA linear EST 18-JUL-2000 ht50905.x1 NCI_CGAP_Mell5 Homo sapiens cDNA clone IMAGE:3150200 3' similar to SW:OX40_HUMAN P43489 OX40L RECEPTOR PRECURSOR ;contains MER22_t1 PTR5 repetitive element ; mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tumor Gene Index
Unpublished (1997)
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NCI-GGAP http://www.ncbi.nlm.nih.gov/ncicgap.
NCI-GGAP http://www.ncbi.nlm.nih.gov/ncicgap.
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Seq primer: -40UP from Gibco
                                                                                                                                          Similarity
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                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
/db_xref="taxon:9606"
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/clone_lib="NCI_CGAP_Mel15"
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                        /lab_host="DH10B"
                                                                                                                                         46.8%;
                                                                                                                                          Score 495; DB 10;
Pred. No. 3.8e-77;
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                                                                                                                                                                                                                                                                                                                                                                  The sequence contained an oligo-dT track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this my represent a bonafide poly A tail. cDNA Library Preparation: M.B. Soares Lab Clone distribution NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            471 bp mRNA linear EST 16-JAN-1
UI-H-B12-ahq-a-02-0-UI.S1 NCI_CGAP_Sub4 Homo sapiens cDNA clone
IMAGE:2727458 3', mRNA sequence.
AW293499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy
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/db_xref="taxon:9606" / db_xref="taxon:9606" / db_xref="taxon:9606" / clone="IMAGE:2727458" / clone=lib="NCI_CGAP_Sub4" / clone_lib="NCI_CGAP_Sub4" / lab_host="DHIBB (Life Technologies)" / lab_host="DHIBB (Life Technologies)" / lab_host="note" pT73D-Pac (Pharmacia) with a modified / note="Vector: pT73D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; The NCI_CGAP_Sub4 library is a subtracted library derived from the NCI_CGAP_Sub1 library which is a subtracted library derived from BI. BI constitutes a mixture of 21 normalized or subtracted NCI_CGAP
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                                                             atgcccacaagccccctgggggaggcagtttccggacccccatccaagaggagcaggccg
                                                                                                                                    ATGCCCACAAGCCCCCTTGGGAGGCAGTTTTCCGGGCCCCCATCCAAAAAGGAGCAGGCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Seq primer: -40UP from Gibco
High quality sequence stop: 217.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nlh.gov

This clone is available royalty-free through LLNL; contact the

IMAGE Consortium (info@image.llnl.gov) for further information.

Insert Length: 797 Std Error: 0.00
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wu42d05.xl Soares_Dieckgraefe_colon_NHCD Homo sapiens cDNA clone
IMAGE:2522897 3' similar to SW:OX40_HUMAN.P43489 OX40L RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished (1997)
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EST.
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1 (bases 1 to 668)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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/clone="IMAGE:2522697"
/clone_lib="Soares_Dieckgraefe_colon_NHCD"
/tissue_type="colonic mucosa from 3 patients with Crohn's disease"
                                                                                                                                                                                                                                                                                                                                                                                                                                                       double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization. Tissue samples provided by Dr. Brian Dieckgraefe (Washington University, dieck@im.wustl.edu); colonic mucosa represents a range of disease involvement from moderate to severe Crohn's disease; samples include both perforating (fistulas) and non-perforating samples. Library constructed by Bento Soares and M. Fatima Bonaldo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /lab_host="DH10B (phage-resistant)"
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Pred. No. 3.4
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                                                                                              gccatcctgctggccctgtacctgctccggagggaccagaggctgccccccggatgccc-a 766
                                                                                                                                                   GGGCCATCGGTTGCCGCCATCCTGGGCCTGGGCCTGGTGCTGAGGCTGACTGGCCCCCTG 339
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 CAAGACCCCTGGGGGAGGCAGTTTCCGGACCCCCATCCAAGAGGAGCAGGCCGACGCCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: L. Jeffrey Medeiros, M.D.,
Emmert-Buck, M.D., Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 398)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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similar to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               www-bio.llnl.gov/bbrp/image/image.html
Seq primer: -40m13 fwd. ET from Amersh
High quality sequence stop: 180.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cDNA Library Preparation: Stratagene, Inc.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (1997)
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                                                                                                                                                                                                                                                                                                                                                       /tissue_type="kidney tumor"
/lab_host="SOLR (kanamycin resistant)"
/note="Organ: kidney; Vector: Bluescript SK-; Site_1:
ECORI; Site_2: XhoI; Cloned unidirectionally. Primer:
Oligo dT. Pooled kidney tumors. 5' adaptor sequence: 5'
GAATTCGGCACGAG 3' 3' adaptor sequence: 5'
CTCGACGTTTTTTTTTTTTTTTTT 3' Average insert size: 1.0 kl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone_lib="NCI_CGAP_Kid6"
/sex="mixed"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
/db_xref="taxon:9606"
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UI-H-BI2-agd-b-03-0-UI.S1 NCI_CGAP_Sub4 Homo sapiens cDNA clone
IMAGE:2723669 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: cgapbs-r@mail.nlh.gov
The sequence contained an oligo-dT track that was present in the
oligonucleotide that was used to prime the synthesis of first
strand cDNA and therefore this may represent a bonafide poly A
tail cDNA Library Preparation: M.B. Soares Lab Clone distribution:
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Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
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National Cancer Institute, Cancer Genome Anat
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//Clone_lib="NCI_CGAP_Sub4"
//clone_lib="NCI_CGAP_Sub4"
//clone_lib="NCI_CGAP_Sub4"
//lab_host="DH10B (Life Technologies)"
//lab_host="DH10B (Life Tech
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/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ggaccagaggctgccccccgatgcccacaagccccctgggggaggcagtttccggacccc 799
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                Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                  Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 347)
                                                                                                                                                                                                                                                                                                                                                                                                    tj50f10.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens IMAGE:2144971 3' similar to contains MER22 t3 MER22
Insert Length: 1030
                                                                                                                                                   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP).
                                                                                                                                                                                                                                                                                                                                        AI452801.1 GI:4287894
                                                                                                                                                                                                                                                                                                                                                                               element ;, mRNA sequence.
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NCI_CGAP_Lu5 pool 1 : LLAM 3575-3582, 3851-3854 (IMAGE CloneIDs 1414920-1417991, 1520904-1522499) NCI_CGAP_GC4 pool 1 : LLAM 3164-3167, 3716-3720, 3733-3735 (IMAGE CloneIDs 1257096-1258631, 1469064-14470983, 1475592-1476743 ) NCI_CGAP_FC2 pool 1 : LLAM 2457-2459, 2758-2759, 3062-3068 (IMAGE CloneIDs 98508-986759), 101192-1101959, 3062-3068 (IMAGE CloneIDs 98508-986759), 101192-1101959, 1217928-1220615) NCI_CGAP_CO10 pool 1 : LLAM 2644-2653, 2871-8872 (IMAGE CloneIDs 1057416-1061255, 1144584-1145351) Subtraction was performed as previously described [Bonaldo, Lennon & Soares (1996): Normalization and Subtraction: Two Approaches To Facilitate Gene Discovery. Genome Research 6, 791-806.]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TAG_LIB=NCI_CGAP_Lei2
TAG_TISSUE=leiomyosarcoma
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Pred. No. 4.8e-44;
0; Mismatches 1
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                                                                                                                                                                                                                                                                                                                                                                                                 ggaccacaataaaaaccttggcag
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 393)
Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fuldner,R.A., Bult,C.J., Lee,N.H., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D., Whi
                                                                                                                                                                                                                                           AA306055 393 bp mRNA linear EST 18-APR-: EST177040 Jurkat T-cells VI Homo sapiens cDNA 5' end similar to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Seg primer: -400F Irom with High quality sequence stop:
                                                                                                                                                       EST
                                                                                                            Homo sapiens
                                                                                                                                   human.
                                                                                                                                                                         AA306055.1 GI:1958383
                                                                                                                                                                                                                    similar to OX40 homolog, mRNA sequence
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/clone="IMAGE:2144971"
/clone_lib="Soars=_NSF_F8_9W_OT_PA_P_S1"
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Pred. No. 8.6e-43;
0; Mismatches 9;
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                                                                                                                                                                                ccgggcgggcacccagcccctggacagctacaagcctggagttgactgtgccccctgccc 400
                                                                                                                                                                                                                                                GGCTGGGAAGCACCCTGCAGCCGGCCAGCAATAGCTCGGACGCAATCTGTGAGGACAG
                                                                                                                                                                                                                                                                         ggctgggaagcacaccctgcagccggccaagcaatagctcggacgcaatctgtgaggacag
                                                                                                                                                                                                                                                                                                                                                              | tecagggcacttcttcccaggcgacaaccaggcctgcaagccctggaccaactgcacctt 460
                                                                                                                                                                                                                                                                                                                                                                                                                            CCGGGCGGCACCCAGCCCCTGGACAGCTACAAGCCTGGAGTTGACTGTGCCCCCTGCCC
                                                                                                                                                           TCCAGGGCACTTCTCCCCAGGCGACAACCAGGCCTGCAAGCCCTGGACCAACCTT
AA501118 630 bp mRNA linear EST 01-JUL-1997 vf97h05.rl Soares_mammary_gland_NbMMG Mus musculus cDNA clone IMAGE:851769 5' similar to gb:Z21674 M.musculus Ox40 (MOUSE);, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          For clone availability, additional sequence and expression information related to this EST, please check the TIGR Human Gene Index (http://www.tigr.org/tdb/hgi/hgi.html)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence Nature 377 (6547 Suppl), 3-174 (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bioinformatics
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: arkerlav@tigr.org
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/db_xref="taxon:9606"
/clone_lib="Jurkat T-cells VI"
/cell_type="T-lymphocyte"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
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                                                                                                                                                                                                        270 tggtgtaacctcagaagtgggagtgagcggaagctgtgcacggccacacaggacaca 329
                                                                                                                                                                                                                                                                                                      210 ccgtgcgggccgggcttctacaacgacgtggtcagctccaagccgtgcaagccctgcacg
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  GACTGTGTTCCCTGCCCTCCTGGCCACTTTTCTCCAGGCCAACACCCAGGCCTGCAAGCCC
                     gactgtgccccctgccctccagggcacttcttcccaggcgacaaccaggcctgcaagccc
                                                                                         GTCTGCAGATGTAGACCAGGCACCCAACCTCGGCAAGACAGCGGCTACAAGCTTGGAGTT
                                                                                                               9tctgccgctgcggggcacccagcccctgga-----cagctacaagcctggagtt
                                                                                                                                                                                  CAGTGCAACCATCGAAGTGGAAGTGAACTCAAGCAGAATTGCACACCTACTCAGGATACT 128
                                                                                                                                                                                                                                                                              CAGGGTGAGACTGGCTTCTACAATGAAGCTGTCAATTATGATACCTGGCAGCAGTGTACA
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AA501118.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tel: 314 286 1800
Fax: 314 286 1810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Marra M/Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished (1996)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Seq primer: -28ml3 rev2 ET from Amersham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: mouseest@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       constructed and normalized by Bento Soares and M Fatters Bonaldo."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="Organ: mammary gland; Vector: pT7T3D-Pac (Pharmacia ) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:851769"
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/dev_stage="4 weeks"
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                                                                                                                                                                                                                                                                                                                               Unpublished (1996)
Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
WashIngton University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Lo
Tel: 314 286 1810
Fax: 314 286 1810
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Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubi
Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,
Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.
Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
Waterston, R.
The WashU-HHMI Mouse EST Project
                                                                                                                                                                                                                         Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:34838
This clone was previously sequenced on the 5' end only, this new
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AI323590 609 bp mRNA linear EST 23-DEC-1998 mp61a10.x1 Soares_thymus_2NbMT Mus musculus cDNA clone IMAGE:573690 3' similar to gb:X85214 M.musculus cx40 gene (MOUSE);, mRNA
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                                                                                                                                                                                  clone was previously sequenced is from the 3' end quality sequence stop: 456.
                              /organism="Mus musculus"
/strain="057BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:573690"
/clone=1ib="Soares_thymus_2NbMT"
                 /sex="male"
                                                                                                                                                                Location/Qualifiers
'tissue_type="Thymus"
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                                                                                                                                                                                                                                                                ggtggacgctgggccccg 881
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                                                                                                                       AI914208
AI914208.1
                                                                                                             EST.
                                     Homo sapiens
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
1 (bases 1 to 247)
                                                                                                                                                              AI914208
wd76e10.xl NCI_CGAP_Lu24
           NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap
National Cancer Institute, Cancer Genome Anal
                                                                                                                                                    mRNA sequence.
Tumor Gene Index
                                                                                               human.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3/]; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pTTT3 vector. RNA provided by Dr. Bertrand Jordan. Library went through two rounds of normalization, and was constructed by Bento Soares and M.Fatima Bonaldo."

a 142 c 197 g 121 t 10 others
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/lab_host="DH10B"
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o sapiens
                                                   Craniata; Vertebrata; Catarrhini; Hominidae;
                                                                                                                                                                               mRNA
                                                                                                                                                                 NA linear EST 17-DEC-1999 CDNA clone IMAGE:2337546 3',
           Anatomy Project (CGAP),
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Best Local Similarity 96.9
Matches 221; Conservative
                                                                                           source
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                                                                                                                                                                                                                                                                                                                                 951
                                                                                                                                                                        CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 373 Std Error: 0.00
Seq primer: -40UP from Gibco.
Location/Qualifiers
1. .247
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Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
/db_xref="taxon.9606"
/clone="IMAGE:2337546"
/clone="IMAGE:2337546"
/clone=lib="NCI_CGAP_LU24"
/tissue_type="carcinoid"
/lab_bost="PH10B"
/lab_bost="PH10B"
/note="Organ: lung; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Plasmid DNA from the normalized library NCI_CGAP_LU5 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDs l141920-1417991 and 1520904-1522439). Subtraction by Bento Soares and M. Fatima Bonaldo. "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   41
                                                                                                                                                                                                                                                                                                                                                                                                                                 19.5%;
                                                                                                                                                                                                                                                                                                                                                                                                               Score 206.4; DB 9; Length 247; Pred. No. 9.1e-27; 0; Mismatches 6; Indels 1
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Result
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Perfect score:
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Copyright (c) 1993 - 2000 Comp
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                                       ACT-4 cell surface
ACT-4 h-1 receptor
Human Ox-40 cDNA.
Plasmid pDC406/Ox4
Ox40/Fc cDNA. Syn
Mouse type-II memb
Mouse Ox40 extrace
                                                                                                                                                                                                                    Description
Tumour suppressor Oligonucleotide fo
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ID AAQ8
  RESULT
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4.9	5.0	5.0	5.0	5.2	5.3	5. ₃	5.3	ა ა	5.3	5.3	5.3	5. 3	5. 3	5.3	5.3	5.3	5 3	5.3	5.3	5.3	5.3	5.3	5.3	5. 3	ω	σ	4	G	9.6	10.3		٠	10.3	0	0
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5	AAQ05620	AAD17186	AAH26499	AAA53209	AAH26495	AAZ37764	AAA50306	AAC97479	AAC91469	AAC90566	AAF30057 '	AAC85433	AAC85947	AAD01240	AAA77604	AAC58596	AAA99903	AAX87670	AAZ37763	AAA50305	AAV19153	AAZ37762	AAA50304	AAA58588	AAZ49948	AAX53491	AAX53491 .	AAS46586	AAS46585	AAS46581	AAH24543	AAH24477	AAH24886	AAH24544	AAH24478
	S	Streptomyces nours	low d	Monkey Fas ligand	Human low density	TR11SV2 nucleotide	Human tumour necro	Human angiogenesis	Human PRO364 cDNA.	PRO36		\Box	e sequen			Human PRO364 prote	0	Human TNF receptor	TR11SV1 nucleotide	Human tumour necro	Nucleotide sequenc	Tumour necrosis fa	Human tumour necro	DNA encoding tumou	Human molecule ass	Human adenosine Al	a	-		r suppresso	secondary		3	secondary	

ALIGNMENTS

(BECT) BECTON DICKINSON CO Cell surface receptor; ACT-4; T-lymphocyte; T-cell; immune system; /*tag= b 1042..1047 93US-0147784 94WO-GB02415 /*tag= 15..86 Location/Qualifiers

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Matches 1056;
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DB; AAR74737.
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antigen activated T-cells, especially, for example, CD4+ T-cells. human cDNA encoding the human OX-40 homologue was cloned as follow Using the Experimental Autoimmune Encephalomyelitis model in rats the OX-40 antigen was identified (expressed on the surface of activated autoantigen-specific CD4+ T-cells present at the site of inflammation but absent on CD4+ T-cells at non-inflammatory sites) and cDNA encoding the antigen was isolated. PCR primers were designed and used to clone murine OX-40 cDNA by PCR from RNA isolated from murine CD4+ T-cells activated with concentrative.
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multiple
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                                                                                                                                                            Nucleic acid encoding an activated T-cell antigen, Ox-40 - used develop prods. for detection and therapy of conditions mediated activated T-cells, eg. multiple sclerosis, rheumatoid arthritis
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                                                                                                                                                                                                                                               Sequence 1317
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428; Conser
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ID AAV3
XX AAV3
AC AAV3
AC AAV3
AC OX4C
KW OX4C
KW OX4C
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                                                                                                                                                                                                                                                                       Synthetic.
Chimeric -
Chimeric -
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23-JUL-1993;
                  22-JUN-1995;
                                  21-JUL-1998
                                                  US5783665-A
                                                                                              mutation
                                                                                                                               mutation
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                                                                                                                                                                                           misc_feature
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                                                                                                   /note= "changed mutant"
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Best Local Similarity 66.0
Matches 428; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  fusion protein that contains the extracellular domain of mouse OX40 fused to the mutated Fc region of the human IgG1 antibody. The fusion protein was used for detecting cDNA clones encoding an OX40 ligand. The invention claims for a murine OX40-L cytokine (AAW48975) that binds to the murine T cell antigen, OX40. The OX40-L protein is claimed to be useful for co-stimulation of T-cell production and in binding assays for detecting OX40 or its homologues. The OX40-L protein is also claimed to generate a TH-2 immune response.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1998-427099/36
DB; AAW48976.
ctggtgctggggctgctgggccccctggccatcctgctggccc
                                                                                                                                                             ccctggaccaactgcaccttggctgggaagcacaccctgcagccggccagcaatagctcg
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                                                                                                                                                                                                                                                                                                                    acagtctgccgctgccgggcgggcacccagcccctgga----cagctacaagcctgga
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       accytyacygygyctccactytytcygygyacacctaccccaycaacyaccygtyctyccac
                                                      tccacccggcccgtggaggtccccggggggccgtgcggttgccgccatcctgggcctgggc
                                                                                                        ccggccaggcccatcactgtccagcccactgaagcctggcccagaacctcacagggaccc
                                                                                                                                             gacgcagtctgtgaggacagaagcctcctggccacactgctctgggagacccagcgccct
                                                                                                                                                                                                 actgtctgcagatgtagaccaggcacccaacctcggcaggacagcggctacaagcttgga
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                                                                                                                                                                                                                                                                                                                                                                                                                 catcogtgtgagactggcttctacaatgaagctgtcaattatgatacctgcaagcagtgt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gagtgccagccaggccatggtatggtgaaccgctgtgatcataccagggatactctatgt
                                      tctacacccaccttggtggagcccagatcttgtgacaaaactcacacatgcccaccgtgc
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Pred. No. 1.5e-43;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             241 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RG
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Best Local S
Matches 394
                                                                                                                                                                                                                                                                                                                                                         glycoprotein
                                                                                                                                                                                                                                                                                                                                                                                                              New isolated DNA encoding the OX40 ligand polypeptide - also vectors and host cells, used to produce recombinant ligand used in e.g. prim. T cell culture, to modulate immune response etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus
                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                        This sequence encodes the extracellular domain of OX40, a men
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23-JUL-1993;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mouse
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es 394; Conserv
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DB; AAR81881.
          gttgactgtgccccctgccctccagggcacttcttcccaggcgacaaccaggcctgcaag
                                                                                                                                                                                                                       acagcaaggcggctcaactgtgttaaacatacctaccccagtggtcacaagtgctgtcgt 120
                                                      acagtctgccgctgccgggcgggcacccagcccctgga-----cagctacaagcctgga
                                                                                     acacagtgcaaccatcgaagtggaagtgaactcaagcagaattgcacacctactcaggat
                                                                                                  acgtggtgtaacctcagaagtgggagtgagcggaagctgtgcacggccacacaggac
                                                                                                                                             cgtccgtgcgggccgggcttctacaacgacgtggtcagctccaagccgtgcaagccctgc
                                                                                                                                                                            gagtgccagccaggccatggtatggtgaaccgctgtgatcataccagggatactctatgt
                                                                                                                                                                                         gagtgcaggccaggcaacgggatggtgagccgctgcagccgctcccagaacacggtgtgc
                                                                                                                                                                                                                                   accgtgacggggctccactgtgtcggggacacctaccccagcaacgaccggtgctgccac 146
grtgactgtgttccctgccctcctggccacttttctccaggcaacaaccaggcctgcaag
                                         actgtctgcagatgtagaccaggcacccaacctcggcaggacagcggctacaagcttgga
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                                                                                                                                                                                                                                                                   Score 283.2; DB 16;
Pred. No. 6.4e-43;
0; Mismatches 158;
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                                                                                                                                                                                                                                                                                                                         151 G; 132 T; 0 other;
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                          The present sequence represents the mouse OX40 extracellular domain encoding cDNA. The extracellular domain of OX40 is its ligand binding domain. The present cDNA was used in the construction of the chimeric OX40/Fc cDNA (AAV32640). The invention claims for a murine OX40-L cytokine (AAW48975) that binds to the OX40 murine T cell antigen. The OX40-L protein is claimed to be useful for co-stimulation of T-cell production and in binding assays for detecting OX40 or its homologues. The OX40-L protein is also claimed to generate a TH-2
                                                                                                                                            Purified polypeptide OX-40 ligands production and binding assays for C
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22-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                   OX40; cytokine; OX40/Fc; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAV32640 standard;
                                                                                                                                                                                         WPI; 1998-427099/36.
                                                                                                                                                                                                                                 (IMMV ) IMMUNEX CORP
                                                                                                                                                                                                                                                                                     22-JUN-1995;
                                                                                                                                                                                                                                                                                                         21-JUL-1998
                                                                                                                                                                                                                                                                                                                               US5783665-A
                                                                                                                                                                                                                                                                                                                                                                                                               Mus sp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mouse OX40 extracellular domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAV32640;
                                                                                                                           Example 1; Col 31-32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25-SEP-1998
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                  response
                                                                                                                                                                               AAW48977
                                                                                                                                                                                                              Fanslow WC,
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95US-0494574.
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/product=
/note= "CD
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1..618
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                                                                                                                                                                                                                                                                                                                                                                                                                                             antigen;
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Sequence

618 BP;

148

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187

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151

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132

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DB 19;

618;

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ARSULT 8
AAS46582/c
ID AAS46582;
XX AC AAS46582;
XC AAS46582;
XX 18-DEC-200
XX 18-DEC-200
XX Human; tun
KW cancer; tu
KW cytosine n
XX WO20016891
XX WO20016891
XX WO20016891
XX 15-MAR-200
PR 06-APR-200
PR 06-APR-200
PR 07-APR-200
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Best I
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                                  15-MAR-2000;
06-APR-2000;
07-APR-2000;
30-JUN-2000;
                                                                                                                   15-MAR-2001;
                                                                                                                                                  20-SEP-2001
                                                                                                                                                                                 WO200168912-A2
                                                                                                                                                                                                                                                cytosine methylation; ds.
                                                                                                                                                                                                                                                                   cancer; tumour;
                                                                                                                                                                                                                                                                                   Human; tumour suppressor gene; oncogene; antitumour;
                                                                                                                                                                                                                                                                                                                                                    18-DEC-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ccctggaccaactgcaccttggctgggaagcacaccctgcagccggccagcaatagctcg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9ttgactgtgcccctgccctccagggcacttcttcccagggcgacaaccaggcctgcaag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cgtccgtgcgggccgggcttctacaacgacgtggtcagctccaagccgtgcaagccctgc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ccggccaggcccatcactgtccagcccactgaagcctggcccagaacctcacagggaccc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gttgactgtgttccctgccctcctggccacttttctccaggcaacaaccaggcctgcaag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 actgtctgcagatgtagaccaggcacccaacctcggcaggacagcggctacaagcttgga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  acagtctgccgctgccgggcgggcacccagcccctgga-----cagctacaagcctgga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   acgtggtgtaacctcagaagtgggagtgagcggaagctgttgcacggccacacaggac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                catccgtgtgagactggcttctacaatgaagctgtcaattatgatacctgcaagcagtgt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gagtgccagccaggccatggtatggtgaaccgctgtgatcataccagggatactctatgt
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       tccacccggcccgtggag
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                                                                                                                                                                                                                                                                                                                suppressor
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                                                                                                                                                                                                                                                                                                                                                                                                                  standard; DNA; 6080
               2000DE-1013847.
2000DE-1019058.
2000DE-1019173.
2000DE-1032529.
2000DE-1043826.
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                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                   2001WO-EP02955
                                                                                                                                                                                                                                                                 CpG dinucleotide; single-nucleotide
                                                                                                                                                                                                                                                                                                                gene derived chemically modified sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26.8%;
70.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    618
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Pred. No. 6.4e-43;
0; Mismatches 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length
                                                                                                                                                                                                                                                                polymorphism;
                                                                                                                                                                                                                                                                                   cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6;
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                                                                                                                                                                                                                                                                 SNP;
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The invention relates to a nucleic acid comprising a sequence of 18 CC bases, of a segment of chemically pretreated DNA (CP DNA) e.g. with CC bisulphite, of genes associated with tumour suppression and CC oncogenes having a sequence taken from 536 (actually 533 since CC numbers 408, 458 and 500 are missing from the sequence listing) sequences CC (SS) and sequences complementary to (SS). The nucleic acid may be a CC peptide nucleic acid-oligomer (PNA) of at least 9 nucleotides and may CC form part of a set of probes for detecting the cytosine methylation state CC and/or single nucleotide polymorphisms and also to be used in an CC array for analysing diseases associated with CpG dinucleotides e.g. CC cancers and tumours. The probes can also be used in a method for CC ascertaining genetic and/or epigenetic parameters for the diagnosis and compared to another set of genetic and/or epigenetic parameters may be CC diseases, by analysing cytosine methylations. The parameters may be CC compared to another set of genetic and/or epigenetic parameters, the CC diseases, by analysing cytosine methylations. The parameters which CC are disadvantageous to patients. The present sequence is one of the CC complementary sequences derived from tumour suppressor genes and CC complementary sequence of the corresponding odd numbered sequence (e.g. cmplementary sequence of the corresponding odd numbered sequence (e.g. cm sisting).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fragments of chemically modified genes associated with tumour suppressor genes and oncogenes, useful in designing primers and probes for analysing diseases associated with cytosine methylation state e.g. cancer
                                                          of the printed specification, format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim
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                                        ftp.wipo.int/pub/published_pct_sequences
                                                                                                                            is missing)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A
                                                                                 The sequence data for this patent did not form e printed specification, but was obtained in ele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ۲,
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                                                                                 orm part
electronic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sequences
                                                                                                                                                   sequence
                                                                                                                                                                                                                                                           which
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Вb
                                                             Query Match
Best Local Similarity
Matches 169; Conser
                                6080
                892
                                               832
CCCTAACCAAAATCTAACC-TAAACCCACAAAATAAACGCTAAACCCCGCCAAACTAAA
                                         Conservative
                                                                     11.8%;
                                                             Score 124.4;
Pred. No. 4.3e
0; Mismatches
                                                              0;
                                                              4.3e-14;
ches 56;
                                                               Indels
                                                              1;
                                                              Gaps
                                6022
5962
                951
                                               891
                                                               1;
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Qy

Sequence 6080

BP; 1124 A;

278

C; 1963 G;

2715

Ή., 0

other

ġ

DB 22;

Length

6080;

5901 1012 5961 CCATACATACCTCCTACCCCGCGAAACCACAATAAAAACCTTAACA ccatgcatacctcctgccccgcgggaccacaataaaaaccttggca 1057 AAACCAACTCTACACCGTTCTAAATACCGATAACTACCTCCGACTCTCTACTTACGTATA gggccaactctgcaccgttctaggtgccgatggctgcctcccggctctctgcttacgtatg 5856

5902 1011

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RESULT 9
AAH24887/c
ID AAH248
XX
AC AAH248
AC AAH248
XX
DT 22-AUG
XX
DT 21-AUG
XX
DT 01igon
 Oligonucleotide
                      22-AUG-2001
                                           AAH24887;
                                                               AAH24887
                                                                standard;
                      (first
 for a secondary signalling motif.
                                                                DNA;
                      entry)
                                                                117
                                                                ВP
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RESULT 10
AAH24478/c
ID AAH244
XX
AC AAH244
XX
AC AAH244
XX
DT 07-AUG
XX',
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                                                                                                                                                                                                                                                                                                                                                                                                          secondary signalling sequences. The specification describes stimulatory corrections y signalling motifs. Primary motifs are efficient at at mediating immune cell signal transduction, particularly when incorporated in an intracellular signalling domain of a chimeric receptor. The primary signalling motif can be combined in any way so as to achieve the desired level of activation (or inhibition) of a number of secondary messenger cascades. The signalling motifs are useful for the primary signalling motifs are useful for the number of secondary messenger cascades. The signalling motifs are useful for the number of secondary messenger of medicament for treating or preventing disease in humans or animals. They are are useful for treating thuman patients suffering from infectious diseases e.g. human patients suffering from infections, inflammatory/autoimmune diseases usuch as asthma and eczema, congenital diseases e.g. cystic fibrosis, sichle cell anemia dermatological diseases e.g. psoriasis, neurological diseases e.g. multiple sclerosis, transplant-related disease e.g. organ transplant rejection, graft versus host disease, metabolic/diopathic
                                                                                                                                                                                                                                                                                                                      Matches
                  07-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Stimulatory primary signalling motif; immune cell; signal transduction; chimeric receptor; inflammatory disease; authimane disease; asthma; eczema; congenital disease; cystic fibrosis; sickle cell anemia; dermatological disease; psoriasis; neurological disease; multiple sclerosis; transplant-related disease; metabolic disease; organ transplant rejection; graft versus host disease; idiopathic disease; diabetes; cancer; ss.
                                                                                      AAH24478
                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Oligonucleotides AAH24886-87 were used to construct DNA encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel cytoplasmic signalling protein and chimeric receptor protein, useful for treating HIV infection, asthma, eczema, psoriasis, multiple scierosis, contain non-natural stimulatory primary signalling motif -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (CELL-) CELLTECH CHIROSCIENCE
                                                                                                                                                                                                             795
                                                                                                                                                                                                                                                  116
                                                                                                                                                                                                                                                                                   735
                                                                                                                                                                              56
                                                                                                                                                                                           acccccatccaagaggagcaggccgacgccactccaccctggccaagatctgacc 850
                                                                                                                                                                                                                                                                 cggagggaccagaggctgcccccgatgcccacaagccccctgggggaggcagtttccgg 794
                                                                                                                                                                                                                                              CGGAGGGACCAGAGGCTGCCCCCGATGCCCAAAAGCCCCCTGGGGGAGGCAGTTTCCGG
                                                                                                                                                                                                                                                                                                                    al Similarity
113; Conser
                                                                                    standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fig
                                                                                                                                                                                                                                                                                                                      Conservative
                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                          B₽;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3; 45pp;
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                                                                                                                                                                                                                                                                                                                                                                                                          11
                                                                                      DNA;
                                                                                                                                                                                                                                                                                                                                                                                                        ۶,
                                                                                                                                                                                                                                                                                                                                    10.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            English.
                                                                                                                                                                                                                                                                                                                                                                                                        Ç
                                                                                                                                                                                                                                                                                                                                                                                                                                           cancer.
                                                                                                                                                                                                                                                                                                                Score 111.2;
Pred. No. 1.1e
0; Mismatches
                                                                                                                                                                                                                                                                                                                    0,
                                                                                                                                                                                                                                                                                                                                                                                                        45
                                                                                                                                                                                                                                                                                                                                                                                                        <u>ن</u>
                                                                                                                                                                                                                                                                                                                                                                                                        26 T;
                                                                                                                                                                                                                                                                                                                                      .1e-11;
                                                                                                                                                                                                                                                                                                                                                                                                        0 other;
                                                                                                                                                                                                                                                                                                                                                       DB
                                                                                                                                                                                                                                                                                                                                                   22;
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                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                   Length 117;
                                                                                                                                                                                                                                                                                                                    0,
                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                         The invention relates to novel primary signalling motifs containing care consensus amino acid sequence. These motifs are extremely efficient at mediating immune cell signal transduction, particularly contents of a consensus amino acid sequence. These motifs are extremely contents of a chimeric contents. Nucleic acids that encode, and polypeptides that contain, contents of these primary signalling motifs are useful in medicine and research. Contents of the contain of the manufacture of a medicament for contrating or preventing disease in humans or in animals. These diseases include infections (e.g. HIV (human immunodeficiency virus) infection), contains (e.g. treating or preventing diseases (e.g. asthma or eczema), congenital continuation or autoimmune diseases (e.g. asthma or eczema), congenital continuation or sichle cell anaemia), dermatological contents, organ transplant rejection or graft-versus-host disease, or metabolic/diopathic diseases (e.g. diabetes or cancer). The construction of sequence blocks (SBs) of primary and secondary in the construction of sequence blocks (SBs) of primary and secondary continuation of the T cell receptor (TCR) complex. Secondary continuations of the transplant respector (TCR) complex. Secondary continuations of continuations of the construction of the continuations of signalling capacity to a continuation of the continuations of the con
                                                                                                                                                                                Query Match
Best Local S
Matches 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New nucleic acids encoding polypeptides with expanded primary signaling motifs, for use in gene therapy, particularly for treating or preventing infections, inflammations or autoimmune diseases in humans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; primary signalling motif; sequence block; SB; immunosuppressiv secondary signalling sequence; antinicrobial; antinflammatory; dermatological; neuroprotective; cytostatic; anti-HIV; antiasthmatic; antistckling; antipsoriatic; antidiabetic; gene therapy; diabetes; immune cell signal transduction; infection; inflammation; cancer;
                                                                                                                                                                                                                                                                                                         Sequence 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      organ transplant rejection; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-2000; 2000WO-GB04193
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       autoimmune disease; congenital disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human secondary signalling
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example
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                                         795
                                                                                          116
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56
                                                                                      cggagggaccagaggctgcccccgatgcccacaagccccctgggggaggcagtttccgg 794
                 acccccatccaagaggagcaggccgacgccactccaccctggccaagatctgacc
                                                                                                                                                                                     al Similarity
113; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      , MH
                                                                                                                                                                                                                                                                                                                                                     impart secondary or le in T cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2; Fig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lawson ADG
                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                         BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3; 43pp; English.
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                                                                                                                                                                                                                                                                                                         Α,
                                                                                                                                                                                                           10.5%;
                                                                                                                                                                                                                                                                                                      35 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         motif SB34 oligo F1340B
                                                                                                                                                                                Score 111.2;
Pred. No. 1.1e
0; Mismatches
                                                                                                                                                                                     0,
                                                                                                                                                                                                                                                                                                         45
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                                                                                                                                                                                                                                                                                                         26 T; 0 other;
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                                                                                                                                                                                                              .le-11;
                                                                                                                                                                                                                                  DB 22;
                                                                                                                                                                                     Indels
                                                                                                                                                                                                                               Length 117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          immunosuppressive;
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                                                                                                                                                                                     Gaps
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RESULT 11 AAH24544/c

AAH24544 standard; DNA; 117

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                                                                                                                                                                              The invention relates to a novel nucleic acid encoding an adaptor CC receptor protein comprising an extracellular ligand-binding domain, a CC transmembrane domain and an intracellular signalling domain. The CC intracellular signalling domain comprises the cytoplasmic portion of at least one adaptor protein, and the extracellular ligand-binding domain CC is not CD8 or a major histocompatibility complex (MHC) class I protein. CC in therapy. They are useful in the mucleic acid encoding it are useful in the adaptor receptor protein and the nucleic acid encoding it are useful in the treatment or prevention of disease in humans and animals. They are useful in the treatment of infectious diseases (e.g. HIV infection), CC inflammatory and autoimmune diseases (e.g. HIV infection), CC congenital diseases (e.g. cystic fibrosis and sickle cell anaemia), CC dermatological diseases (e.g. psoriasis), neurological diseases (e.g.) CC multiple sclerosis), organ transplant rejection, graft-versus-host CC disease and metabolic/idiopathic diseases such as diabetes and cancer. CC The present sequence is one of a large number of oligonucleotides used in the construction of sequence blocks (SBs) of primary and secondary csignalling motifs transduce either a construction of rCCR) complex. Secondary signalling motifs impart CC cells. Primary and secondary signalling capacity to a molecule in T CC components of the adaptor receptor protein of the invention.
                                                                    Query Match
Best Local S
Matches 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel polynucleotide encoding adaptor receptor protein useful for treating human immunodeficiency virus (HIV) infection, asthma, cy fibrosis, multiple sclerosis, organ transplant rejection, diabete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        neurological disease; organ transplant rejection; diabetes; cancer; graft-versus-host disease; adaptor receptor protein; sequence block; SB; primary signalling motif; secondary signalling motif; ss.
                                                                                                                                                        Sequence 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Finney HM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (CELL-) CELLTECH CHIROSCIENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            autoimmune disease; cystic fibrosis; sickle cell anaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            antisickling; antipsoriatic; neuroprotective; immunosuppressive;
antidiabetic; cytostatic; HIV infection; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human secondary signalling motif SB34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       08-AUG-2001
   116
                                   735
                cggagggaccagaggctgccccccgatgcccacaagccccctgggggaggcagtttccgg 794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sapiens.
CGGAGGGACCAGAGGCTGCCCCCGATGCCCAAAAGCCCCCTGGGGGAGGCAGTTTCCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                anti-HIV; antiinflammatory; antiasthmatic; dermatological;
                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fig
                                                                      Conservative
                                                                                                                                                        BP;
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                                                                                                                                                      11 A;
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                                                                                    10.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           English.
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                                                                    0;
                                                                                    Score
Pred.
                                                                                                                                                        45
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                                                                  Mismatches
                                                                                    111.2;
No. 1.1
                                                                                                                                                      26
                                                              . 1.1e-11;
3;
                                                                                                                                                      T; 0 other;
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                                                                    Indels
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                                                                    0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cystic
57
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735

cggagggaccagaggctgcccccgatgcccacaagccccctgggggaggcagtttccgg

Matches Query Match Best Local :

Local Similarity

10.3%; 99.1%;

Score 109.4; Pred. No. 2.3

.3e-11; DB 22;

Conservative

0,

Mismatches

Indels Length 117;

0

Gaps 794

0

Sequence 117

BP;

25

Α.

45 C;

36 G;

11 T; 0 other;

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RESULT 1
AAH24886
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                                                                                                                                                                                     secondary signalling sequences. The specification describes stimulatory primary signalling motifs. Primary motifs are efficient at at mediating immune cell signal transduction, particularly when incorporated in an intracellular signalling domain of a chimeric receptor. The primary signalling motif can be combined in any way so as to achieve the desired level of activation (or inhibition) of a number of secondary messenger cascades. The signalling motifs are useful in therapy and in the manufacture of medicament for treating or preventing disease in humans or animals. They are are useful for treating human patients suffering from infectious diseases e.g. human immunodeficiency virus (HIV) infections, inflammatory/autoimmune diseases such as actions of creating such as actions of control of the series and control o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          multiple sclerosis; transplant-related disease; metabo organ transplant rejection; graft versus host disease;
                                                                         such as asthma and eczema, congenital diseases e.g. cystic fibrosis, sickle cell anemia, dermatological diseases e.g. psoriasis, neurological diseases e.g. multiple solerosis, transplant-related disease e.g. organ transplant rejection, graft versus host disease, metabolic/idiopathic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel cytoplasmic signalling protein and chimeric receptor protein, useful for treating HIV infection, asthma, eczema, psoriasis, multiple sclerosis, contain non-natural stimulatory primary signalling motif -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        chimeric receptor; inflammatory disease; autoimmune disease; ast eczema; congenital disease; cystic fibrosis; sickle cell anemia; dermatological disease; psoriasis; neurological disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Oligonucleotide for a secondary signalling motif.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAH24886
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Oligonucleotides AAH24886-87 were used to construct DNA encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Stimulatory primary signalling motif; immune cell; signal transduction;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     idiopathic disease; diabetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (CELL-) CELLTECH CHIROSCIENCE
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                                                    e.g.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fig 3; 45pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lawson ADG;
                                                    diabetes, and cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
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AAB244477
ID AAH244477
ID AAH244477
AX AAH24447X
AX O7-AUG
AX O7-A
                                                                                                    signalling motifs. Primary signalling motifs are sequences that transduce either a stimulatory or an inhibitory signal, which regulates primary activation of the T cell receptor (TCR) complex. Secondary motifs impart secondary or co-stimulatory signalling capacity to a
                                                                                                                                                                                                                                        sclerosis), organ transplant rejection or graft-versus-host disease metabolic/idiopathic diseases (e.g. diabetes or cancer). The present sequence is one of a large number of oligonucleotides used the construction of sequence blocks (SBs) of primary and secondary
                                                                                                                                                                                                                                                                                                                                                                            when incorporated into an intracellular signalling domain of a chimeric receptor. Nucleic acids that encode, and polypeptides that contain, these primary signalling motifs are useful in medicine and research. They are useful in therapy, or in the manufacture of a medicament for treating or preventing disease in humans or in animals. These diseases include infections (e.g. HIV (human immunodeficiency virus) infection), inflammatory or autoimmune diseases (e.g. asthma or eczema), congenital diseases (e.g. cystic fibrosis or sickle cell anaemia), dermatological diseases (e.g. psoriasis), neurological diseases (e.g. multiple
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to novel primary signalling motifs containing a consensus amino acid sequence. These motifs are extremely efficient at mediating immune cell signal transduction, particularly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New nucleic acids encoding polypeptides with expanded primary signaling motifs, for use in gene therapy, particularly for treating or preventing infections, inflammations or autoimmune diseases in humans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2001-328791/34.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (CELL-) CELLTECH CHIROSCIENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAH24477;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 795
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                                                                           impart secondary or le in T cells.
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RESULT 14
AAH24543
CC receptor protein comprising an extracellular ligand-binding domain, a comprising an extracellular signalling domain. The CC intracellular signalling domain and comprise the cytoplasmic portion of at CC least one adaptor protein, and the extracellular ligand-binding domain comprise to me adaptor protein, and the extracellular ligand-binding domain comprise to me adaptor protein, and the nucleic acid encoding it are useful comparts of the construction of the respy. They are useful in the manufacture of a medicament for the creatment or prevention of disease in humans and animals. They are useful in the manufacture of a medicament for the creatment of infectious diseases (e.g. HIV infection), comparts of infections diseases (e.g. asthma and eczema), compenital diseases (e.g. cystic fibrosis and sickle cell anaemia), compenital diseases (e.g. cystic fibrosis and sickle cell anaemia), compenital diseases (e.g. poriasis), neurological diseases (e.g.) compenital diseases (e.g. meurological diseases (e.g.) corgan transplant rejection, graft-versus-host compensation of sequence blocks (SBs) of primary and secondary signalling motifs transduce either a construction of sequence blocks (SBs) of primary and secondary signalling motifs transduce either a construction or an inhibitory signal, which regulates primary activation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel polynucleotide encoding adaptor receptor protein useful for treating human immunodeficiency virus (HIV) infection, asthma, cystic fibrosis, multiple sclerosis, organ transplant rejection, diabetes and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               autoimmune disease; cystic fibrosis; sickle cell anaemia; psoriasis; neurological disease; organ transplant rejection; diabetes; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             antisickling; antipsoriatic; neuroprotective; immunos
antidiabetic; cytostatic; HIV infection; inflammation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example
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Pred. No. 2.
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07-APR-2000;
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                                                                                                                                                                                                                                                                                                                                                                       genes and analysing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI;
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                                         The invention relates to a nucleic acid comprising a sequence of 18 bases, of a segment of chemically pretreated DNA (CP DNA) e.g. with bisulphite, of genes associated with tumour suppression and oncogenes having a sequence taken from 536 (actually 533 since numbers 408, 458 and 500 are missing from the sequence listing) sequences; and sequences complementary to (Ss). The nucleic acid may be a peptide nucleic acid-oligomer (PNA) of at least 9 nucleotides and may form part of a set of probes for detecting the cytosine methylation; and/or single nucleotide polymorphisms and also to be used in an analyor strategy and detecting the cytosine methylation; and the sequence is a sequence of the cytosine methylation is analyor single nucleotide polymorphisms and also to be used in an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Olek
                                                                                                                                                                                                                                                                                                        Claim 1;
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                            analysing diseases associated with CpG
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                                                                                                                                                                                                                                                                                                                                                                Note: The sequence data for this patent did not form of the printed specification, but was obtained in eleformat directly from WIPO at
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Patent: US 5821332-A 1 13-OCT-1998;
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Location/Qualifiers
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                                                                                                                       /db_xref="taxon:9606"
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/protein_id="AABB33944.1"
/protein_id="AABB33944.1"
/db_xref="GI:913406"
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P(NTARTLGRGPCAALLLLGLGLSTVTGLHCVGDTYPSNDRCCHECR
P(NTARTLGRACTQFLDSYKPGVDCAFCPFGHFSPGDNQACKFWTNCTLAGKHTLQPASNSSD
AICEDRDPPATQPQETQGPPARPITVQPTEAWPRTSQGPSTRPVEVPGGRAVAAILGL
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/note="cell surface
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                                              tggacgctgggccccgccaggctggagcccggagggtctgctggggggagcagggcaggtt
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1 (bases 1 to 1358)

Latza,U., Durkop,H., Schnittger,S., Ringeling,J., Eitelbach,F., Hummel,M., Fonatsch,C. and Stein,H.

The human OX40 homolog: CDNA structure, expression and chromosoma assignment of the ACT35 antigen
Eur. J. Immunol. 24 (3), 677-683 (1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (16-DEC-1993) U. Latza, FU Berlin, Klinikum Steglitz, Institute of Pathology, Hindenburgdamm 30, 12200 Berlin, FRG Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                 /translation="MCVGARRLGRGPCAALLLLGLGLSTVTGLHCVGDTYPSNDRCCH ECRPGNGMVSRCSRSQNTVCRPCGPGFYNDVVSSKPCKPCTWCNLRSGSERKQLCTAT QDTVCRCRGAGTQPLDSYKPGVDCAPCPPGHFSPGDNQACKPWTWCTLAGKHTLQPASN SSDAICEDRDPATQPQETQGPPARPITVQPTEAWPRTSQGPSTRPVEVPGGRAVAAI LGLGLVLGLLGPLAILLALYLLRRDQRLPPDAHKPPGGGSFRTPIQEEQADAHSTLAK I"
                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product="OX40 homologue"
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/db_xref="GI:472958"
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The human OX40 homolog: CDNA structure, expression assignment of the ACT35 antigen
Eur. J. Immunol. 24 (3), 677-683 (1994)
                                                 and Bulfone-Paus, S. The HTLV-I tax protein
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AJ277151.1 GI:8926701
CD134 antigen; OX40 gen
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/number=7
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2717. .27
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CDTVCRCRAGTQPLDSYKPGVDCAPCPPGHFSPGDNQACKPMTNCTLAGKHTLQPASN
SSDAICEDRDPPATQPQETGQPPARPITVQPTEAMPRTSQGPSTRPVEVPFGGRAVAAI
IGLGLVIGLLGPLAILLALYLLRRDQRLPPDAHKPPGGGSFRTPIQEEQADAHSTLAK
I"
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/gene="ox40"
3930. .4096
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3719. .3796
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/db_xref="taxon:9606"
join(1267. .1437.1635. .1757,2328. .
join(1267. .1437.1635. .1757. .4096)
3284. .3480,3590. .3718,3797. .4096)
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/gene="ox40"
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3797. .40
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/gene="ox40"
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/gene="ox40"
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Best Local S
Matches 207
                                                                                                                                              AUTHORS
TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GCGGGACCACAATAAAAACCTTGGCAG 4076
                                                                                  Homo sapiens chromosome 1 clone RP5-902P8, PROGRESS ***, 4 unordered pieces.
                              Web site: http://www.sanger.ac.uk
Contact: humquery@sanger.ac.uk
                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                               Homo sapiens
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HTG; HTGS_PHASE1; HTGS_ACTIVEFIN; HTGS_DRAFT; HTGS_FULLTOP
Center project name: dJ902P8
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/gene="ox40"
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1672 c 1755 g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /gene="ox40"
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                        Project Information
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0; Mismatches
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*** SEQUENCING IN
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21484
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  GCGGGACCACAATAAAAACCTTGGCAG
                      gcgggaccacaataaaaaccttggcag 1058
                                                                                                                                                                                     gagcagggcaggtgcaggccgcctgcccgccacgctcctgggccaactctgcaccgttc 971
                                                                                  TAGGTGCCGATGCCTCCCGGCTCTCTGCTTACGTATGCCATGCATACCTCCTGCCCC
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                                                                                                                                                                          GAGCAGGGCAGGTGCAGGCCTGCCCCGCCACGCTCCTGGGCCAACTCTGCACCGTTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Insert size: 110819; sum-of-contigs
Insert size: 160089; 6.7% error; agarose-fp
Quality coverage: 8.36x in Q20 bases; sum-o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               coverage: 5.95x in Q20 bases; agarose-fp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NOTE: This is a 'working draft' sequence. It currently consists of 4 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22049
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43086 549:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="assembly_fragment:00075
fragment_chain:1"
67355. .111119
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fragment_chain:1"
55038. .67254
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/db_xref="taxon:9606"
/chromosome="1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone="RP5-902P8"
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L. .42985
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ragment_chain:1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 42985: contig of 42985 bp in length 1085: gap of 100 bp 54937: contig of 11852 bp in length 1037: gap of 100 bp 10549; contig of 12217 bp in length 1354: gap of 100 bp 111119: contig of 43765 bp in length
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                                                                                                                                                                                                                                                                                                                                               0;
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21458
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1.9e-93;
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                                                                                                                                                                                                                                                                                                                                                                                     Length 111119;
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KEYWORDS
SOURCE
ORGANISM
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AUTHORS
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AL390719
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JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Assembly program: XGAP4; version 4.5
Sequencing vector: plasmid; LO8752; 100% of reads
Chemistry: Dye-terminator ET-amersham; 2% of reads
Dye-terminator Big Dye; 97% of reads
Consensus quality: 201072 bases at least Q40
Consensus quality: 204266 bases at least Q30
Consensus quality: 204043 bases at least Q20
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AL390719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Insert size: 208144; sum-of-contlys
Insert size: 227650; 6.6% error; agarose-fp
Quality coverage: 5.63x in Q20 bases; sum-o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk On Feb 1, 2002 this sequence version replaced gi:16304463.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HTG;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         * arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown
* This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               * NOTE: This is a 'working draft' sequence. It currentl
* consists of 29 contigs. The true order of the pieces
* is not known and their order in this sequence record
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Web site:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Center: Wellcome Trust Sanger Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (24-JAN-2002) Wellcome Trust Sanger Institute, Hinxton
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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60772
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51493 60771: con
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8189 23213: contig of 8088 bp in length
23214 23313: gap of 15025 bp in length
23314 27320: contig of 300 bp in length
27221 27320: gap of 100 bp
27321 30326: contig of 3006 bp in length
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                                                                    72 63164: contig of 2293 bp

55 63264: gap of 100 bp

55 6397: contig of 6043 bp

7647: gap of 100 bp

7647: contig of 7240 bp
    cont
; gap of
98297; cr
18 98397;
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                                                                                                                                                                                                                              43166: contig of 12740 bp in length
43266: gap of 100 bp
47516: contig of 4250 bp in length
47616: gap of 100 bp
51392: contig of 3776 bp in length
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fragment_chain:2"
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ragment_chain:1"
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ragment_chain:2"
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Query Match 19.6%; Score 207; DB 2; Best Local Similarity 100.0%; Pred. No. 1.8e-93; Matches 207; Conservative 0; Mismatches 0;
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1032 gcgggaccacaataaaaaccttggcag 1058
                                                taggtgccgatggctgcctccggctctctgcttacgtatgccatgcatacctcctgcccc 1031
                                                                                                GAGCAGGGCAGGTGCAGGCCGCCTGCCCGCCACGCTCCTGGGGCCAACTCTGCACCGTTC
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137975. .147639
/note="ass--''
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206963. .210944
/note="assembly_fragment:04407"
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AX134865.1
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1 (bases 1 to 117)
Finney, H.M. and Lawson, A.D.
Polypeptides with expanded primary signalling motifs
Patent: WO 0132867-A 73 10-MAY-2001;
Celltech Chiroscience Limited (GB)
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Sequence 73 from Patent W00132867.
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Finney, H.M. and Lawson, A.D.
Polypeptides with non-natural primary
Patent: WO 0132709-A 58 10-MAY-2001;
Celltech Chiroscience Limited (GB)
Location/Qualifiers
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/db_xref="taxon:32630"
/note="Chimeric receptor construction oligonucleotide F1340A"
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1 (bases 1 to 117)
Finney, H.M. and Lawson, A.D.
Hybrid adaptor receptors
Patent: WO 0132866-A 88 10-MAY-2001;
Celltech Chiroscience Limited (GB)
Location/Qualifiers
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                                                                                                             artificial sequence.

1 (bases 1 to 117)
Finney,H.M. and Lawson,A.D.
Folypeptides with non-natural primary signalling
Patent: WO 0132709-A 59 10-MAY-2001;
Celltech Chiroscience Limited (GB)
Coation/Qualifiers
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Sequence
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Sequence 59 from Patent
AX134866
AX134866.1 GI:14271354
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                                                              /organism="synthetic construct"
/db_xxef="taxon:32630"
/note="oligonucleotide for chim
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/db_xref="taxon:32630"
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1 (bases 1 to 17)
Finney, H.M. and Lawson, A.D.
Polypeptides with expanded primary signalling motifs
Patent: WO 0132867-A 74 10-MAY-2001;
Celltech Chiroscience Limited (GB)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AX134963 117 bp
Sequence 74 from Patent W00132867.
AX134963
AX134963.1 GI:14271405
                                                                                                                                      Finney, H.M. and Lawson, A.D.
Hybrid adaptor receptors
Patent: WO 0132866-A 89 10-MAY-2001;
Celltech Chiroscience Limited (GB)
                                                                                                                                                                                   artificial sequence.
1 (bases 1 to 117)
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Sequence 89 from Patent W00132866.
AX135076
AX135076.1 GI:14271471
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                                                       /organism="synthetic construct"
/db_xref="taxon:32630"
/note="Adaptor receptor constuct
F1340B"

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/db_xref="taxon:32630"
/note="Chimeric receptor construction F1340B"
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32; Conserv
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1 (bases 1 to 1358)

Latza, U., Durkop, H., Schnittger, S., Ringeling, J., Eitelbach, F., Hummel, M., Fonatsch, C. and Stein, H.

The human OX40 homolog: cDNA structure, expression and chromoson assignment of the ACT35 antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (16-DEC-1993) U. Latza, FU Berlin, Klinikum Steglitz, Institute of Pathology, Hindenburgdamm 30, 12200 Berlin, FRG Location/Qualifiers
1. .1373
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814. .958
959. .1079
1341. .1346
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ECRPGNGMVSRCSRSQNTVCRPCGPGFYNDVVSSKPCKPCTWCNLRSGSERKQLCTAT
QDTVCRCRAGTQPLDSYKPGVDCAPCPPGHFSPGDNQACKPWTNCTLAGKHTLQPASN
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/product="0X40 homologue"
/protein_id="CAA53576.1"
/protein_id="GI:472988"
/db_xref="SWISS-PROT:P43489"
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LGLGLVLGLLGPLAILLALYLLRRDQRLPPDAHKPPGGGSFRTPIQEEQADAHSTLAK
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/db_xref="taxon:9606"
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1 (bases 1 to oir),

Baum, P.R., Fanslow, W.C. III, oir,

Cytokine which is a ligand for OX40

Patent: US 5783665-A 6 21-JUL-1998;

Location/Qualifiers

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Baum, P.R., Fanslow, W.C. III, Gayle, R
Cytokine which is a ligand for 0x40
Cytokine which is a ligand for 0x40
Patent: US 5457035-A 6 10-0CT-1995;
Location/Qualifiers
                                                                                                                          Z21674
Z21674.1
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114933
114933.1
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Musinae; Loases 1 to 883)
Calderhead,D.M., Buhlmann,J.E., van den Eertwegh,A.J., Claassen,E. Noelle,R.J. and Fell,H.P.
Cloning of mouse Ox40: a T cell activation marker that may mediate T-B cell interactions
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and for OX40
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Sequence
AR019521
                                                                                    1 (bases 1 to 1317)
Baum, P.R., Fanslow, W.C. III, Gayle, R.B.
Cytokine which is a ligand for OX40
Patent: US 5783665-A 10 21-JUL-1998;
Location/Qualifiers
1. .1317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (11-FEB-1993) David M Calderhead, Molecular Im
Bristol-Myers Squibb, Pharmaceutical Research Institute,
Ave., Seattle, WA, 98121, USA
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            Similarity
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/db_xref="taxon:10090"
/clone="pUCOx40.RJ.1"
/cell_line="TH2 D.10"
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/strain="Balb/c"
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                                                                                                                                                                                                                                                                                                                            Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; I
Mammalla; Butheria; Rodentia; Sciurognathi; Muridae;
1 (bases 1 to 2907)
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X85214
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Baum, Panslow, W.C. III, Gayle, R.B.
Cytokine which is a ligand for OX40
Patent: US 5457035-A 10 10-OCT-1995;
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Birkeland, M.L.
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                                                                                                                                                                                                                                                                          of rat 0X40 protein
                                                                                                                                                                                                                                                                                          Gene
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                      join(180. .312,534. .656,1208.
2472. .2591,2680. .2750)
/gene="ox40"
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1. .1317
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                                                                                     /organism="Mus musculus"
/db_xref="taxon:10990"
join(<1..312,534..656,1208.
2472..2591,2680..2907)
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AC100470/c
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AC100470.1 GI:17047836
HTG; HTGS PHACED
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; E
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
1 (bases 1 to 60953)
Birren,B., Linton,L., Nusbaum,C. and Lander,E.
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                                                    Mus musculus
                                                             house mouse.
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657. .120
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/db_xref="GI:732819"
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/codon_start=1
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LOW-PASS SEQUENCE SAMPLING
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COMMENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lamazares, R., Landers, T., Lehoczky, J., Levine, R., Liu, G., MacLean, C., Macdonald, P., Major, J., Marquis, N., Matthews, C., MacCarthy, M., McEwan, P., McKernan, K., McPheeters, R., Meldrim, J., Mcneus, L., Mihova, T., Mienga, V., Murphy, T., Naylor, J., Nguyen, C., Morbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P., Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P., Raymond, C., Retta, R., Rieback, M., Santos, R., Schauer, S., Schupback, R., Seman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schupback, R., Semann, S., Severy, P., Spencer, B., Stange-Thomann, N., Storauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Travis, N., Trigilio, J., Vessillev, H., Volan, M., Malan, J., Wall, N., Wall, J., Young, G., Walson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Valler, N., Wall, M., N., Willian, M., Ye, W.J., Young, G., Valler, M., Volan, M., Volan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N., Anderson,S., Barna,N., Bastien,V., Boguslavkiy,L., Boukhgalter,B. Brown,A., Camarata,J., Campopiano,A., Chang,J., Chazaro,B., Choepel,Y., Colangelo,M., Collins,S., Collymore,A., Cook,A., Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S., Dodge,S., Faro,S., Ferreira,P., FitzHugh,W., Gage,D., Galagan,J., Gardyna,S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (22-NOV-2001) Whitehead Institute/MIT Center Research, 320 Charles Street, Cambridge, MA 02141, USA All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Zainoun, J., Zembek, L., Zimmer, A. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ginde, S., Gord, S., Goyette, M., Graham, L., Grand-Plerre, N., Hagos, B., Heaford, A., Horton, L., Hulme, W., Illev, I., Johns Jones, C., Kamat, A., Karatas, A., Kells, C., LaRocque, K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus, clone RP23-139J18
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                    sequencing reads that have not been assembled into contigs. Runs of N are used to separate the reads and the order in which they appear is completely arbitrary. Low-pass sequence sampling is useful for identifying clones that may be gene-rich and allows
                                                                                                                                                                                                                                                                                                                                            be preserved.
                                                                                                                                                                                                                                                                                                                                                                        overlap relationships among clones to be deduced. However, it should not be assumed that this clone will be sequenced to completion. In the event that
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                                                                                                                                                                                                                                                                                                                                                           the record is updated,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: sequence_submissions@genome.wi.mit.edu
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2 4751: contig

2 4851: gap of

2 5561: contig

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17727: contig of
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1356: gap of 2
25072: cc-
172:
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36463: contig
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14: gap
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33996: contig of
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28288: contig of
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14492: contig of
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16917: contig of 697 bp
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RESULT 2
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                   Direct Submission
Submitted (26-OCT-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 15A, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Nov 2, 2001 this sequence version replaced gi:16416310.
                                                                                                                                                                                                                                                                                                                                                                                                                                     AL627204 253111 bp DNA linear HTG 27-0 Mus musculus chromosome 4 clone RP23-118E21, *** SEQUENCING
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                                                                                                                                                                   Sims, S
                                                                                                                                                                                                                                                                      Mus musculus
                                                                                                                                                                                                                                                                                                                            AL627204.5 GI:16596721
HTG; HTGS_PHASE1; HTGS_DRAFT
                                                                                                                                                                                                                                                                                                                                                                                                           PROGRESS ***, in unordered pieces.
                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                     house mouse.
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41487 42162; contig of 676 bp in length
42163 42262; gap of 100 bp
42263 42983; contig of 721 bp in length
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18 54419: contig of 702 bp in 14
20 54519: gap of 100 bp
20 55229: contig of 710 bp in 14
30 55329: gap of 100 bp
30 55329: gap of 100 bp
30 56023: contig of 694 bp in 14
24 56123: gap of 100 bp
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43809; cor
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2 52077: gap of 100 bp

52077: gap of 100 bp

52796: contig of 719 bp in length

52896: gap of 100 bp

53617: contig of 721 bp in length

53717: gap of 100 bp

54419: contig of 721 bp
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49506: contig of 693 bp in length
49606: gap of 100 bp

50333: contig of 727 bp in length
50433: gap of 100 bp

51151: contig of 718 bp in length
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39779: contig
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this sequence version replaced gi:16416310 Genome Center
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; Pred. No. 0.0041;
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fragment_chain:3
clone_end:T7
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fragment_chain:1"
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Sequencing vector: plasmid; LO8752; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of reads Consensus quality: 250604 bases at least Q40 Consensus quality: 251169 bases at least Q30 Consensus quality: 251526 bases at least Q20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Center code: SC

Center code: SC

Web site: http://www.sanger.ac.uk

Contact: humquery@sanger.ac.uk

Contact: humquery@sanger.ac.uk
                                                                                                       Insert size: 252011; sum-of-contigs
Insert size: 263925; 8.0% error; agarose-fp
Quality coverage: 11.85x in Q20 bases; sum-of-contigs Quality
coverage: 11.37x in Q20 bases; agarose-fp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Center: Sanger Centre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Center project name: bM118E21
                                                                                                                                                                                                                                                                                                                                                                                                                                     Assembly program: XGAP4; version
NOTE: This is a 'working draft' sequence. This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Summary Statistics
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/chromosome="4" /db_xref="taxon:10090" organism="Mus musculus" Cocation/Qualifiers it is available and the accession number will

vector_side:left" 23722. .26584 clone_end:SP6 /note="assembly_fragment:05628 fragment_chain:1 /note="assembly_fragment:07355 fragment_chain:1" /clone="RP23-118E21" /clone_lib="RPCI-23"

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fragment_chain:2"
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fragment_chain:2"
124655. .138457 61416. .124554 /note="assembly_fragment:00235 fragment_chain:2" /note="assembly_fragment:01898
fragment_chain:2" .61315

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FOCUS

/note="assembly_fragment:00567
fragment_chain:2"
179139. .210421 224120. .227775
/note="assembly_fragment:01289
fragment_chain:3"
fragment_533111
227876. .253111 /note="assembly_fragment:07085 fragment_chain:2" /note="assembly_fragment:00017
fragment_chain:2" ragment_chain: .224019

ector_side:right" 61670 c 60569 g 64276 t 1108 others

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1221 others

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Length 254197; Indels

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Gaps

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PUBMED
REFERENCE
AUTHORS
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Matches 28; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       St. Philadelphia, PA 19104, USA

* NOTE: This is a 'working draft' sequence. It currently
consists of 13 contigs. Gaps between the contigs
are represented as runs of N. The order of the pieces
is believed to be correct as given, however the sizes
of the gaps between them are based on estimates that have
provided by the submittor.

* This sequence will be replaced
by the finished sequence as soon as it is available and
the accession number will be preserved.

1 32448: contig of 32448 bp in length
32549 32548: gap of unknown length
56901 57000: gap of unknown length
115351 11350: contig of 58350 bp in length
115351 113450: gap of unknown length
115351 11346: contig of 58350 bp in length
11846: contig of 58350 bp in length
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21635547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Reed,D.K., Li,X., Bachmanov,A.A., Li,S., Chen,Z., Tordoff,M.G., Beauchamp,G.K., de Jong,P.J., Wu,C., Chen,L., West,D.B., Ross,D and Ohmen,J.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Cranlata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 254197)
Li,x., Bachmanov,A.A., Li,S., Chen,Z., Tordoff,M.G., Beauchamp,G.K., de Jong,P.J., Wu,C., Chen,L., West,D.B., Ross,D.A., Ohmen,J.D. and Reed,D.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (08-JUN-2001) Monell Chemical Senses Center, 3500 Market
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 (bases 1 to 254197)
Reed, D.R., Li, X., Bach
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Genetic, physical, and comparative map of the subtelomeric region
of mouse Chromosome 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AF389853 254197 bp DNA linear HTG 24-JAN-2002 Mus musculus chromosome 4 clone RPCI-23-118E21 strain C57BL/6J, WORKING DRAFT SEQUENCE, 13 ordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AF389853.1 GI:18307770
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/ 100.0%; Pr
/ ''va 0;
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254197: contig
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g of 7341 bp in length
of unknown length
g of 21700 bp in length
of unknown length
g of 28982 bp in length
                                               unknown 1
of 26380
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of 2596 bp in length
unknown length
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Kremmidiotis,G., Gardner,A.E., Callen,D.F. and Sutherland,G.R. Direct Submission
Submitted (24-JUN-1999) Cytogenetics & Molecular Genetics, Women's & Children's Hospital, 72 King William Rd, Adelaide, SA 5006,
                                                                                                                                                                                                                                                                                                                                                   SEQUENCE,
AC007905
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  synthetic construct artificial sequence.
1 (bases 1 to 5148)
1 (bases) 1 to 5148)
                                                                                                                                                                                                                                                                                                                                                                                                Homo
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                                                                                                                                        Kremmidiotis,G., Gardner,A.E., Callen,D.F Large Scale Sequencing of the Chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28;
                                                                                                             Unpublished
                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                   AC007905.2 GI:10:
HTG; HTGS_PHASE2;
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                                                                                                                                     Large Scale Sequencing
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/strain="C57BL/6J"
/db_xref="taxon:10090"
/chromosome="4"
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/db_xref="taxon:32630"
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                                                                                                                                     Callen, D.F. and
Chromosome 16 rec
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On Sep 23,
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Centre Code : C
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1 1479: contig of 1479 bp in length
1480: gap of unknown length
1488: 6699: contig of 5212 bp in length
6700: 6707: gap of unknown length
6708: 10905: contig of 4198 bp in length
10913: gap of unknown length
10913: gap of unknown length
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29772: contig (
29779: gap of (
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    60033:
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51206:
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29279: contig of 4412 begin length
29286: gap of unknown length
29772: contig of 486 bp in length
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24860: contig
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20018: contig of 6155 bp in length
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f unknown length
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g of 1710 bp in length
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of 933 bp in length
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of 4819 bp in
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                                                                                                                                                                                                                                                                                                                  Submitted (14-MAY-1997) Takahiro Isono, Shiga University of Medical Science, Central Research Laboratory; Seta Tsukinowachou, Otsu, Shiga 520-2192, Japan (E-mail:isono@belle.shiga-med.ac.jp, Tel:81-775-48-2308, Fax:81-775-48-2048)
                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; C
Mammalia; Eutheria; Lagomorpha;
1 (bases 1 to 877)
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AB003911.1
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/db_xref="taxon:9606"
/chromosome="1624.3"
/clone="RP4-754F33"
a 28756 c 29631 g 22706
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GMVSRCNRSQDTICHPCEPGFYNEAVNYQACKPCTQCNRRSGSEPQQECTHTRDTVCR
CRPGTQPLNGYKHGVDCAPCPQGHFSEGNNRACRPWTNCTLAGKRTLQPASSISDAVC
                                    /product="OX40 precursor"
/protein_id="BAA20059.1"
/db_xref="GI:2114108"
/tb=xref="GI:2114108"
                                                                     /codon_start=1
/product="OX40
                                                                                                                           /cell_type="HTLV-I-transformed T cell"
                                                                                                                                           /db_xref="taxon:9986"
/cell_line="H446"
                                                                                                                                                                                     /strain="Chbb:HM"
                                                                                                                                                                                                                                Location/Qualifiers
                            translation="GLAAALGLALLLLGLLLGAEPRPDCVGDTYPGGDRCCLECQPGY/
                                                                                                                                                                      /sub_species="domesticus"
                                                                                                                                                                                                 organism="Oryctolagus cuniculus"
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Lagomorpha; Leporidae; Oryctolagus
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ig of 14682 bp in length
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                                                                                                                                                                                                                                                                                                                                                                                                                                     web site: http://www.nisc.nih.gov/
Contact: nisc_mgc@nhgri.nih.gov
Shevchenko,Y., Wetherby,K.D., Beckstrom-Sternberg,S.M.,
Benjamin,B., Blakesley,R.W., Bouffard,G.G., Brinkley,C., Brooks,S.,
Bietrich,N.L., Guan,X., Gupta,J., Ho,S.-L., Karlins,E., Legaspi,R.,
Lim,M., Maduro,Q.L., Mastello,C., Mastrian,S.D., McCloskey,J.C.,
McDowell,J., Pearson,R., Snyder,B., Stantripop,S., Thomas,P.J.,
Tiongson,E.E., Touchman,J.W., Tsurgeon,C., Vogt,J.L., Walker,M.A.,
Zhang,L.-H. and Green,E.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1420 bp
Homo sapiens, clone IMAGE:3050476,
BC002494
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
Gaithersburg, Maryland;
Web aito:
                                                                                                                                                                                                                                                                                                                                                         Clone distribution: MGC clone distribution through the I.M.A.G.E. Consortium/LLNL at: Series: IRAL Plate: 4 Row: e Column: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC/DCTD/DTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
Submitted (05-FBB-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Strausberg, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                             passed the following selection criteria: GenomeScan gene
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               /product="Unknown (protein
/protein_id="AAH02494.1"
                                                                                                                      /tlssue_type="Skin, melanotic melanoma."
/clone_lib="NIH_MGC_20"
/lab_host="DH10B-R"__
                                                                                                                                                                                                                                                         1. .1420
                                                           /codon_start=2
                                                                                                  /note="Vector:
                                                                                                                                                                                     /db_xref="taxon:9606"
/clone="IMAGE:3050476"
                                                                                                                                                                                                                                 /organism="Homo sapiens"
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Bandman,O., Tang,K.T., Azimzai,Y., Yue,H., Baughn,M.R., Hillman,J.L., Lal,P., Wang,E., Gandhi,A.R., Policky,J.L. and
                                                                                                                                                                           Homo sapiens mRNA; cDNA
AL137382
AL137382.1 GI:6807912
                                Submitted (15-JAN-2000) MIPS,
                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 1632)
Ansorge,W., Wirkner,U., Mewes,H.W., Well,B. and Wiemann,S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Patent: WO 0153469-A 10 26-JUL-2001; Incyte Genomics, Inc. (US)
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                                               Direct Submission
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PCLVLALVPWAVHMFSAQEAPPIHSS"
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FLGDPKILFLEYEPAAYYASRRVGIAVUMISLITEWILNIFKWELFGORPFWWYHESG
YYSQAPAQVHQEPSSCETGPGSPSGHCMITGAALWPIMTALSSQVATRARSRWVRVWP
SLAYCTFLLAVGLSRIFILAHFPHQVLAGLITGAVLGWLMTPRVPMERBLSFYGLTAL
ALMLGTSLIYWTLFTLGLDLSWSISLAFKWCERPEWIHVDSRPFASLSRDSGAALGLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
/db_xref="taxon:9606"
/db_xref="taxon:9606"
/note="Incyte ID No: 1269556CB1"
/note="Incyte ID No: 357 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
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S. Wiemann,
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m clone DKFZp434L1226).
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Homo sapiens, clone MGC:31975 IM
BC021574
BC021574.1 GI:18204314
MGC
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German Genome Project.

This clone (DKFZp434L1226) is available at the RZPD in Berlin.

Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 1405

Please contact the RZPD: Brail: clone@tzpd.de Further

That of the RZPD is available at the RZPD in Berlin.
                                                                                                                                                                                                                                                                                                                                                                        cDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Genome Sequence Centre,
BC Cancer Agency, Vancouver, BC, Canada
info@bcgsc.bc.ca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Please contact the RZPD: Ressourcenzentrum, Hevenzerin-Charlottenburg, GERMANY; Email: clone@rzinformation about the clone and the sequencing
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAL Plate: 40 Row: i Column: 5
This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF
                                                                                                                                                       Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield, Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin, Letticia Hsiao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven Ness, Pawan Pandoh, Anna-Liisa Prabhu, Parvaneh Saeedi, Jacqueline Schein, Duane Smailus, Michael Smith, Lorraine Spence, Jeff Stott, Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy, George Yang, Scott Zuyderduyn, Marco Marra.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
Direct Submission
Direct Submission
Submitted (14-JAN-2002) National Institutes of Health, Mammalian Submitted (MGC), Cancer Genomics Office, National Cancer Gene Collection (MGC), Cancer Genomics Office, National Cancer Trastitute. 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de; sequenced by EMBL (European Molecular Biology Laboratories, Heidelberg/Germany) within the cDNA sequencing consortium of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/db_xref="taxon:9606"
/db_ne="Dkr2p434L1226"
/clone=_lb=*434 (synonym: htes3). Vector pSport1; host pH10B; sites Not1 + Sal1"
/dev_stage="adult"
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/map="16q24.3"
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Search completed: June 19, 2002, 02:21:10 Job time: 3946 sec
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Location/Qualifiers
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21; Conservative
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SCETGFGSPSGHCMITGAALWFIMTALSSQVANTRARSKWVRVWESLAYCTFLLAVGLS
RIFILAHFPHQVLAGLLIFGAVLGWAMTPRVFWBERLSSYGLTALALMLGTSLIYWTLF
TLGLDLSWSISLAFKWCERPEWIHVDSRPFASLSRDSGAALGLGIALHSPCYAQVRRA
                                                                                                                                                                                                                                                                                                                 QLGNGQKIACLVLAMGLLGPLDWLGHPPQISLFYIFNFLKYTLWPCLVLALVPWAVHM
                                                                                                                                                                                                                                                                                                                                                                                                         /product="Unknown (protein for MGC:31975)"
/protein_id="AAH21574.1"
/db_xref="G1:18204315"
/translation="MESTLGAGIVIAEALQNQLAWLENVWLWITFLGDPKILFLFYFP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone="MGC:31975 IMAGE:4842511"
/tissue_type="Eye, normal, pigmented retinal epithelium"
/clone_lib="NHH_MGC_43"
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/db_xref="taxon:9606"
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DB seq length: 2000000000
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BI833441 603088995
AW591834 xx86b03.x
BI824093 603039230
BI911081 603068733
AI452801 tj50f10.x
BI821828 603035715
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AI914208 wd76e10.x
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                                                  cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Washington University Genome Sequencing C
Clone distribution: NCI-CGAP clone distribution information
found through the I.M.A.G.E. Consortium/LLNL at:
info@image.llnl.gov
See primer: -40UP from Gibco
High quality sequence stop: 478.
Location/Qualifiers
                                                                                                                                                                Email: cgapbs-r@mail.nih.gov
Tissue Procurement: M. Bento Soares, Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
Bonaldo, Ph.D.
                                                                                                                                                                                                                        Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 569) NCI-CGAP http://www.ncbi.nlm.nih.gov/nclcgap. National Cancer Institute, Cancer Genome Anatomy Project (CGAP), National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                           BG236062 FIG. 369 bp mRNA linear EST 12-FEB-2001 naf22807.x1 Soares_NPBMC Homo sapiens CDNA clone IMAGE:4141716 3' similar to SW::X40_HUMAN P43489 OX40L RECEPTOR PRECURSOR; contains MERC2_t1 TAR1 repetitive element; mRNA sequence.
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BG236062.1 GI:12749909
                                                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4141716"
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BE312775

BM048374

BE312775

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AA312871 EST183529

AI126122 qd77b04 x

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AA477725 zu44f11 s

AA477725 zu44f11 s

AA477725 zu44f1 s

AA477725 zu44f1 s

AI264558 q109f04 x

AI669655 wc12a05 x

BM006189 603614011 br725110 bx12c11 y

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544 bp mRNA linear EST 16-OCT-2000 7h90a10.x1 NCI_CGAP_CO16 HOMO Sapiens CDNA clone IMAGE:3333226 3' similar to SW:OX40_HUMAN P43489 OX40L RECEPTOR PRECURSOR ;contains MER22.tl PTR5 repetitive element ; mRNA sequence.

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Eukaryota;
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 Metazoa; Chordata; Craniata; Vertebrata;
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Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Ilan Kirsch, M.D.,
Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mammalia; Butheria; Primates; Catarrhini; Hom
1 (bases 1 to 544)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cDNA Library Preparation: M. Bento Soares, Ph.D. cDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-GGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL, send email to:
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Seq primer: -40UP from Gibco
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/db_xref="taxon:9606"
/clone="MAGE:3323226"
/clone_lib="NCI_CGAP_C016"
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/lab_host="DH10B"
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99.8%;
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Pred. No. 1.8e-173;
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CTCCGGAGGGACCAGAGGCTGCCCCCGATGCCCACAAGCCCCCTGGGGGAGGCAGTTTC
                                                                506;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: cgapbs-r@mail.nih.gov

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Chris Moskaluk, M.D., Ph.D., Michael R.

Tissue Procurement: Chris Moskaluk, M.D., Ph.D. Life

Emmert-Buck, M.D., Ph.D. cDNA Library Preparation: Life

Technologies, Inc. cDNA Library Arrayed by: Christa Prange,

Technologies, Consortium DNA Sequencing by: Washington Univers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information
found through the I.M.A.G.E. Consortium/LLNL, send email to:
info@image.llnl.gov
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Seq
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NCI-CGAP http://www.ncbi.nlm.nih.gov/nclcgap.
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Location/Qualifiers
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06; Conservative
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Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies."
162 c 200 g 77 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
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/clone_lib="NCI_CGAP_Mel15"
/tissue_type="malignant melanoma, metastatic to lymph
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Pred. No. 4.2e-171;
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Unpublished (1997)
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Robert Strausberg, Ph.D.
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/db_xref="taxon:9606"
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844 bp mRNA linear EST 20-DEC-1999 willd02.xl NCI_CGAP_CO16 Homo sapiens cDNA clone IMAGE:2389923 3' similar to SW:OX40_HUMAN P43489 OX40L RECEPTOR PRECURSOR ; contains MER22.t3 MSR1 repetitive element ;, mRNA sequence.

AI738634
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National Cancer Institute, Cancer Genome Anat
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cDNA Library Arrayed by: Greg Lennon, Ph.D.
cDNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP Clone distribution information can be
                                                        /note="Organ: colon; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Soc RI; Plasmid DNA from the normalized library NCI_CGAP_Col0 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDs 1057416-1061255, and 1144584-1143351).
Subtraction by Bento Soares and M. Fatima Bonaldo. a 245 c 302 g 154 t 4 others
                                                                                                                                                                                                                                                                                                                             /Clone="IMAGE:2389923"
/Clone_lib="NCI_CGAP_Co16"
/tissue_type="colon tumor,
/lab_host="DH10B"
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1 (bases 1 to 393)

RS Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A., Bult, C.J., Lee, N.H., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D., White, C.J., Lee, N.H., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D., White, C.J., Lee, N.H., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D., White, C.J., Sutton, G., Blake, J.A., Brandon, R.C., Man-Wai, C., Clayton, R.A., Cilne, T.R., Cotton, M.D., Earle-Hughes, J., Fine, L.D., Fitzgerald, L.M., Fitzhugh, W.M., Fritchman, J.L., Geoghagen, N.S., Glodek, A., Geehm, C.L., Hanna, M.C., Hedblom, E., Hinkle, P.S., Jr., Kelley, J.M., Kelley, J.M., Kelley, J.M., Kelley, J.M., Merrick, J.M., Merrick, J.M., Moreno-Palanques, R.F., McDonald, L.A., Nguyen, D.T., Pelligrino, S.M., Phillips, C.A., Ryder, S.E., Scott, J.L., Saudek, D.M., Shirley, R., Small, K.V., Spriggs, T.A., Utterback, T.R., Wedman, J.F., Li, Y., Bednarik, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.J., Li, Y., Bednarik, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.J., Hu, J.S., Greene, J.M., Gruber, J., Hudson, P., Kim, A.K., Kozak, D.L., Kunsch, C., Hungjun, J., Li, H., Meissner, P.S., Olsen, H., Raymond, L., Weil, Y.F., Wing, J., Xu, C., Yu, G.L., Ruben, S.M., Dillion, P.J., Fannon
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similar to OX40 homolog, mRNA sequence.
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Mammalia; Eutheria; Primates;
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Tel: 3018699056
Fax: 3018699423
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                                                                                                                                                                                                  AW293499
UI-H-BIZ-ahq-a-02-0-UI.sl NCI_CGAP_Sub4
IMAGE:2727458 3', mRNA sequence.
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Tritial assessment of human gene diversity and based upon 83 million nucleotides of cDNA sequentum 377 (6547 Suppl), 3-174 (1995) 96026280
Contact: Kerlavage, AR
Unpublished (1997)
Contact: Robert St
                              Tumor Gene Index
                                        Mammalia; Eutheria; Primates; Catarrhini; Hor
1 (bases 1 to 471)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap
National Cancer Institute, Cancer Genome Ana
                                                                                                                          Homo sapiens
                                                                                                                                                                   AW293499
AW293499.1 GI:6700135
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The Institute for Ge
9712 Medical Center
                                                                                                         Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: arkerlav@tigr.org For clone availability,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
/db_xref="ATCC (inhost):160207"
/db_xref="taxon:9606"
/clone_lib="Jurkat T-cells VI"
/cell_type="Tymphocyte"
/note="Vector: pBluescript SK-; S.
Xhol"
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strand cDNA and therefore this may represent a bonafide poly A
tail. cDNA Library Preparation: M.B. Soares Lab Clone distribution:
NCI-CGAP clone distribution information can be found through the
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www-bio.llnl.gov/bbrp/image/image.html
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /lab_nost="DHIUB (Life Technologies)"
/note="vector: pPT3D-Pac (pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; The NCI_CGAP_Sub4 library is a subtracted library derived from the NCI_CGAP_Sub2 library which is a subtracted library derived from the NCI_CGAP_Sub1 library, which is a subtracted library derived from the NCI_CGAP_Sub1 library, which is a subtracted library derived from BI. BI constitutes a mixture of 21 normalized or subtracted NCI_CGAP_Pr28, NCI_CGAP_CO4, NCI_CGAP_EC46, NCI_CGAP_EC46, NCI_CGAP_EC46, NCI_CGAP_EC46, NCI_CGAP_EC41, NCI_CGAP_EC41, NCI_CGAP_EC41, NCI_CGAP_EC41, NCI_CGAP_EC41, NCI_CGAP_LU5, NCI_CGAP_CC6, NCI_CGAP_LU5, NC
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TAG_LIB=NCI_CGAP_Lei2
TAG_TISSUE=leiomyosarcoma
TAG_SEQ=AATCG"
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Pred. No. 4.1e-97;
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UI-H-BI2-agd-b-03-0-UI.sl NCI_CGAP_Sub4 Homo sapiens cDNA clone
IMAGE:2723669 3', mRNA sequence.
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Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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                  /note="wector: p7733-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; The NCI_CGAP_Sub4 library is a subtracted library derived from the NCI_CGAP_Sub4 library which is a subtracted library derived from the NCI_CGAP_Sub1 library, which is a subtracted library derived from the NCI_CGAP_Sub1 library, which is a subtracted library derived from BI. BI constitutes a mixture of 21 normalized or subtracted NCI_CGAP_Brid5, NCI_CGAP_CO4, NCI_CGAP_EC2, NCI_CGAP_Kid5, NCI_CGAP_CO4, NCI_CGAP_EC3, NCI_CGAP_Kid1, NCI_CGAP_CO4, NCI_CGAP_EC4, NCI_CGAP_CO5, NCI_CGAP_CO5, NCI_CGAP_LU5, NCI_CGAP_LU2, NCI_CGAP_Brid3, NCI_CGAP_CO8, NCI_CGAP_CO1, NCI_CGAP_Brid3, NCI_CGAP_CO4, NCI_CGAP_LU2, NCI_CGAP_Brid3, NCI_CGAP_CO4, NCI_CGAP_CO4, NCI_CGAP_LU2, NCI_CGAP_LU3, NCI_CGAP_LU3, NCI_CGAP_CO4, NCI_CGAP_CO4, NCI_CGAP_LU3, NCI_CGAP_LU3, NCI_CGAP_EC4, NCI_CGAP_GC6, NCI_CGAP_Brid3, NCI_CGAP_EC4, NCI_CGAP_GC6, NCI_CGAP_Brid3, NCI_CGAP_EC4, NCI_CGAP_GC6, NCI_CGAP_Brid3, NCI_CGAP_EC4, NCI_CGAP_GC6, NCI_CGAP_Brid3, NCI_CGAP_EC4, NCI_CGAP_GC6, NCI_CGAP_EC4, NCI_CGAP_EC4, NCI_CGAP_GC6, NCI_CGAP_EC4, NCI_
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/db_xref="taxon:9606"
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/lab_host="DH10B (Life Technologies)"
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NCI_CGAP_GC4
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nes 207; Conservative (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           mRNA sequence.
BI833441
                                                                                                                                                                                                                                                                                                                                          Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc
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EST.
                                                                                                                                                                                        http://image.llnl.gov
plate: LLAM11571 row: m column:
                                                                                                                                                                                                                                  CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                              NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian
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1 (bases 1 to 743)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   603088095F1 NIH_MGC_120 Homo sapiens cDNA clone IMAGE:5227199
                                                                                                                                                                      High quality sequence stop: 659.
                                                                                                                                                                                                                                                                                                                                                                                      Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               human.
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TAG_LIB-NCI_CGAP_Lei2
TAG_TISSUE-leiomyosarcoma
TAG_SEQ-AATCG"
TAG_SEQ-AATCG
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) NCI_CGAP_Pr22_pool 1: LLAM 2457-2459, 2758-2759,
3062-3068 (IMAGE CIONEIDS 985608-986759, 1101192-1101959,
1217928-1220615) NCI_CGAP_CO10 pool 1: LLAM 2644-2653,
1217928-1220615) NCI_CGAP_CO10 pool 1: LLAM 2644-2653,
2871-2872 (IMAGE CIONEIDS 1057416-1061255, 1144584-1145351)
Subtraction was performed as previously described (Bonaldo, Lennon & Soares (1996): Normalization and
                                                                                    /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                              /clone-"IMAGE:5227199"
                                                                                                                                                Location/Qualifiers
/note="Organ:
                        /lab_host-"DH10B"
                                            /clone_lib-"NIH_MGC_120"
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  and spleen;
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TITLE
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ggccccccggccaggcccatcactgtccagcccactgaagcctggcccagaacctcacag 614
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                                                                                                                                                                                                                                                                                DNA Sequencing by: Washington University Genome Sequencing C Clone distribution: NCI-CCAP clone distribution information found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov/lmage/html/lresources.shtml
Seq primer: -40UP from Gibco
                                                                                                                                                                                                                                                                                                                                                                           Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Life Technologies catalog #: 11547-015
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 198)
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Location/Qualifiers
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National Cancer Institute, Cancer Genome Anat
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 34
/note="Organ: lymph node; Vector: pCMV-SPORT6; SalI; Site_2: NotI; Cloned unidirectionally. For Oligo dT. Average insert size 1.25 kb. Life Tecatalog #: 11547-015" 31 t 1 others
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a 275 c 235 g 98 t
                                                                                                                /tissue_type="lymphoma,
cell"
                                                                                                                                               /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2850509"
/clone_lib="NCI_CGAP_Lym12"
                                                                                               /lab_host="DH10B"
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Best Local Similarity
             Query Match
Best Local Similarity
Matches 142; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         tatgccatgcatacctcctgccccgcgggaccacaataaaaacccttggcag 1058
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         tcctgggccaactctgcaccgttctaggtgccgatggctgcctccggctctctgcttacg 1007
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TCCTGGGCCAACTCTGCACCGTTCTAGGTGCCGATGGCTGCCTCCGGCTCTCTGCTTACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       171;
                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
http://image.llnl.gov
plate: LLAM11449 row: k column: 08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 172)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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High quality sequence stop: 172.
Location/Qualifiers
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Contact: Robert Strausberg, Ph.D.
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             13.4%; ilarity 100.0%; Conservative
                                                                                                             24
                                                                                                      /note="Organ: pooled brain, lung, testis; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA source anonymous pool of 6 male brains, age range 23-27; 1 male lung, age 27; and 1 male testis, age 69. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.8 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 021. Note: this is a NHH_MGC Library."
                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5180287"
/clone_lib="NIH_MGC_115"
                                                                                                                                                                                                                                                                                              /lab_host="DH10B"
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100.0%;
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Pred. No. 8.4e-7
                            Score 142; DB 10;
Pred. No. 3.8e-56;
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sapiens cDNA clone
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IMAGE:5180287 5',
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Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collections, 1 (1000)
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High quality sequence stop: 593.
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                                                                                                                                                                                                                                                                                                                     (Invitrogen). Research Genetics this is a NIH_MGC Library." a 300 c 272 g 150 t
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1.2-3.3 kb.
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/clone_lib="NIH_MGC_118"
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/lab_host="DH10B"
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Email: capabs-remail.nih.gov

This clone is available royalty-free through LLNL; contact the This clone is available royalty-free through LLNL; contact the This clone is available royalty-free through LLNL; contact the This clone is available royalty-free through LLNL; contact the This clone is available royalty-free through LLNL; contact the This clone is available royalty-free through LLNL; contact the This clone is available royalty-free through LLNL; contact the This clone is available royalty-free through LLNL; contact the This clone is available royalty-free through LLNL; contact the This clone is available royalty-free through LLNL; contact the This clone is available royalty-free through LLNL; contact the This clone is available royalty-free through LLNL; contact the This clone is available royalty-free through LLNL; contact the This clone is available royalty-free through LLNL; contact the This clone is available royalty-free through LLNL; contact the This clone is available royalty-free through LLNL; contact the This clone is available royalty-free through LLNL; contact the This clone is available royalty-free through LLNL; contact the This clone is available royalty-free through LLNL; contact the This clone is available royalty-free through LLNL; contact the This clone is available royalty-free through LLNL; contact the This clone is available royalty-free through LLNL; contact the This clone is available royalty-free through LLNL; contact the This clone is available royalty-free through LLNL; contact the This clone is available royalty-free through LLNL; contact the This clone is available royalty-free through LLNL; contact the This clone is available royalty-free through LLNL; contact the This clone is available royalty-free through LLNL; contact the This clone is available royalty-free through LLNL; contact the This clone is available royalty-free through the This clone is available royalty-free through the This clone is available royalty-
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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/db_xref="taxon:9606"
/clone="IMAGE:2144971"
/clone_11b="Soares_NSF_F8_9W_OT_PA_P_S1"
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                                                                                                                                                                                                                                                                                     sequence.
AA970291
                                                                                                                                                                                                                                                                                                                                        op09h05.sl NCI_CGAP_Kid6 similar to SW:OX40_HUMAN
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Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
plate: LLAM11440 row: n column: 04
Unpublished (1997)
                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 398)
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                          Tumor Gene Index
                                                NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap
National Cancer Institute, Cancer Genome Ana
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National Institutes of Health, Mammalian Gene Collection (MGC)
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/clone_11b="NIH_MGC_115"
/lab_host="DH10B"
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Pred. No. 1.3e-3
                                                                                                                                                                                                                                                                                                                                     398 bp mRNA linear EST 20-MAY-1998
Homo sapiens cDNA clone IMAGE:1575225 3'
P43489 OX40L RECEPTOR PRECURSOR;, mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             82;
        cDNA Library Preparation: M. Bento Soares, Ph.D. cDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-GGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html Insert Length: 373 Std Error: 0.00 Seq primer: -400P from Gibco.
                                                                                                                                                                                                                 NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
1 (bases 1 to 247)
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cDNA Library Arrayed by: Greg Lennon, DNA
DNA Sequencing by: Washington University Genome
Clone distribution: NCI-CGAP clone distribution
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
seq_primer: -40ml3 fwd. ET from Amersham
                                                                                                                                                                                        Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
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                                                                                                                                       Tissue Procurement: Christopher Moskaluk, M.D., Emmert-Buck, M.D., Ph.D.
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/sex="mixed"
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/db_xref="taxon:9606"
/clone="IMAGE:1575225"
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IMAGE:2522697 3' similar to SV
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
1 (bases 1 to 668)
                                                                                                                                                                                                                                                                                                             Seq primer: -40UP from Gibco
High quality sequence stop: 217.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
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National Cancer Institute, Cancer Genome Anatomy
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/tissue_type="colonic mucosa from 3 patients with Crohn's disease"
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                                                                                                                                                                                       /clone="IMAGE:2522697"
/clone_lib="Soares_Dieckgraefe_colon_NHCD"
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/db_xref="taxon:9606"
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/clone="IMAGE:2337546"
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W:0X40_HUMAN P43489 0X40L RECEPTOR
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1.5e-16;
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AZ320958
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error:
Plate: 0041 row: A column: 08
Seq primer: CGTTGTAAAACGACGGCCAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished (2000)
Contact: Robert B. Weiss
University of Utah
University of Utah
RMB. 308, Biomedical Polymers Res
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 662)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AZ320958 662 bp DNA linear GSS 29-SEP-200 1M0041A08F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0041A08 F, DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      High quality sequence stop: 662.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Class: plasmid ends
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was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization. Tissue samples provided by Dr. Brian Dieckgraefe (Washington University, dieck@im.wustl.edu); colonic mucosa represents a range of disease involvement from moderate to severe Crohn's disease; samples include both perforating (fistulas) and non-perforating samples. Library constructed by Bento Scares and M. Fatima Bonaldo. "
                                                                                                                                                                                               /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Biomedical Polymers Research Bldg.,
                                                                                                                                                                                                                                                                                               /organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0041A08"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
                                                                                                                                                  Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/).
                                                                                                                                                                                                                                                                                                                                                                                                                                1. .662
                                                                                                                                                                                                                                                                                /sex="Male"
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0; Mismatches
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2.2e-10;
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Best Local S
Matches 28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sequence.
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630 bp mRNA linear EST 01-JUL-1997 vf97h05.rl Soares_mammary_gland_NbMMG Mus musculus cDNA clone IMAGE:851769 5' similar to gb:Z21674 M.musculus Ox40 (MOUSE);, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Marra M/Mouse EST Project
Washu-HHMI Mouse EST Project
Washington University School of Medicinep
4444 Forest Park Parkway, Box 8501, St. Lo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 630)
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
                       RI; 1st strand cDNA was primed with a Not primer (5)
                                                                                  /note="Organ: mammary gland; Vector: pT7T3D-Pac (Pharmacia
) with a modified polylinker; Site_1: Not I; Site_2: Eco
RI; 1st strand cDNA was primed with a Not I - oligo(dT)
                                                                                                                                                                                                                                                                      /organism="Mus musculus
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:851769"
                                                                                                                                                      /dev_stage="4 weeks"
/lab_host="DH10B"
                                                                                                                                                                                                  /tissue_type="mammary gland"
                                                                                                                                                                                                                            /sex="male"
                                                                                                                                                                                                                                               /clone_lib="Soares_mammary_gland_NbMMG"
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double-stranded cDNA was ligated to Eco RI s (Pharmacia), digested with Not I and cloned into
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Matches 21
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Matches
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1 (bases 1 to 342)

Dias Neto,E., García Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H., Brunstein,A., deOllveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
                                                                                                                                                                                                                                                                                                                                                           Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=RC6-NT0029-280
400-012-B08&t3=2000-04-28&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 342.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar,
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RC6-NT0029-280400-012-B08 NT0029
 l Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tel: +55-11-2704922
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            h 2.3%;
Similarity 100.0%;
24; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fax: +55-11-2707001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               144
2.0%; Silarity 100.0%; Conservative 0;
                                                                                                                   83
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                                                                                                           /note="Organ: nervous_tumor; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
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                                                                                                                                                                                                                                                                    /db_xref="taxon:9606"
/clone_lib="NT0029"
/dev_stage="Adult"
                                                                                                                                                                                                                                                                                                                             /organism="Homo sapiens"
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               Score 21;
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                 DB 9;
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                                       Length 342;
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A1823620/c
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sequence.
AA312871
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AI823620.1 GI:5444291
                                     AA312871 480 bp
EST183529 Jurkat T-cells VI Homo
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Insert Length: 811 Std Error: 0.00
Seq primer: -40Up from Glbco
High quality sequence stop: 437.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cDNA Library Preparation: M. Bento Soares, Ph.D. cDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 (bases 1 to 477)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anat
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished (1997)
                                                                                                                                                                                                                                                             Similarity
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                                                                                                                                                                                                                                          Conservative
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                                                                                                                                                                                                                                                                                                                                                                                    /note-*Organ: kidney; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Plasmid DNA from the normalized library NCI_CGAP_Kid5 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDs 1323912-1325831, 1471368-1472903 and 1492104-1493255). Subtraction by Bento Soares and M. Fatima Bonaldo. "
                                                                                                                                                                                                                                                                                                                                                             Fatima Bonaldo.
94 c 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone="IMAGE:2398765"
/clone_lib="NCI_CGAP_Kid12"
/tissue_type="2 pooled tumors (clear cell type)"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                           2.0%;
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                                                                                                                                                                                                                                      0;
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                                   mRNA linear E
sapiens cDNA 5' end,
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                                                          EST 19-APR-1997
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VERSION
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AI126122/c
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C.J., Lee, N.H., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D., White
O., Sutton, G., Blake, J.A., Brandon, R.C., Gocayne, J.D., White
Cline, T.R., Cotton, M.D., Earle-Hughes, J., Fine, L.D., Fitzgerald
L.M., Fitzhugh, W.M., Fritchman, J.L., Geoghagen, N.S., Glodek, A.,
Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle, P.S., Jr., Kelley, J.M.,
Kelley, J.C., Liu, L.-T., Marmaros, S.M., Merrick, J.M.,
Kelley, J.C., Liu, L.-T., Marmaros, S.M., Merrick, J.M.,
Moreno-Palanques, R.F., McDonald, L.A., Nguyen, D.T., Pelligrino, S.M.,
Phillips, C.A., Ryder, S.E., Scott, J.L., Saudek, D.M., Shirley, R.,
Small, K.V., Spriggs, T.A., Utterback, T.R., Weidman, J.F., Li, Y.,
Bednarik, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.J.,
Dimke, D., Feng, D.-F., Ferrie, A., Fischer, C., Hastings, G.A., He, W.W.,
Hu, J.S., Greene, J.M., Gruber, J., Hudson, P., Kim, A.K., Kozak, D.L.,
Wei, Y.F., Wing, J., Xu, C., Yu, G.L., Ruben, S.M., Dillion, P.J., Fannon,
M.R., Rosen, C.A., Haseltine, W.A., Fields, C., Fraser, C.M. and
                                                                                                                                                                                                                                                            TGGGGCTGCTGGCCCCCTGG
                                                                                                 3', mRNA sequence
AI126122
                                                                                                                         482 477b04.x1 Soares_testis_NHT 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: arkerlav@tigr.org
Email: arkerlav@tigr.org
Email: arkerlav@tigr.org
Email: arkerlav@tigr.org
Email: arkerlav@tigr.org
Information related to this EST, please check the TIGR Human
Index (http://www.tigr.org/tdb/hgi/hgi.html)
Eukaryota;
                    Homo sapiens
                                                                            AI126122.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence Nature 377 (6547 Suppl), 3-174 (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Kerlavage, AR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 480)
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                                          human
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/db_xref="AXCC (Inhost):160191"
/db_xref="taxon:9606"
/clone_lib="Jurkat T-cells VI"
/cell_type="T-lymphocyte"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       note="Vector: pBluescript SK-;
Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                            GI:3594636
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Pred. No.
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44;
                                                                                                                                     sapiens
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                                                                                                                                   linear EST 28-OCT-1998 cDNA clone IMAGE:1735471
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AUTHORS
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688 tggggctgctgggccccctgg
                                                                         White,Y., Wylie,T., W
WashU-NCI human EST P
Unpublished (1997)
Contact: Wilson RK
                                Washington University Scho
                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 545)

Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S., Krizman, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Marti, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B., White, Y., Wylie, T., Waterston, R. and Wilson, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome
Clone distribution: NCI-CGAP clone distribution
found through the I.M.A.G.E. Consorttum/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 723 Std Error: 0.00
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AA477725.1 GI:2206359
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1 (bases 1 to 482)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cDNA Library Preparation: M. Bento Soares, Ph.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
314 286 1800
314 286 1810
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/db_xref="taxon:9606"
/clone="IMAGE:1735471"
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                                                                                                                                                                                                                                                                        Contact: Genoscope
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1 (bases 1 to 572)
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                                                                                                                                                                                                                       Email: segref@genoscope.cns.fr,
                                                                                                                                                                                                                                                     Genoscope - Centre National de Sequencage
                                                                                                                                                                                                                                                                                                                                                                                                       human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This clone is available royalty-free through LLNL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: est@watson.wustl.edu
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117 c 204 g 103 t 1 others
           /note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
/db_xref="GDB:5940824"
/db_xref="taxon:9606"
/clone="IMAGE:740877"
 vector
                                                                                                           /clone="CSODC004YD06"
/clone_lib="LTI_NFL003_NBC3"
/sex="male"
                                                                                                                                                         /organism="Homo sapiens"
/db_xref="taxon:9606"
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                                                                            /tissue_type="neuroblastoma cells"
/lab_host="DH10B"
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by Life Technologies

Contact : Feng Liang

Query Match Best Local Similarity

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
                                                                                                                                                                                                                                                                                                                                                                                 Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtm12.p17t1-CM28t2-CM2-CI0179-
181100-528-f10&t3-2000-11-18&t4-1)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tel: +55-11-2704922
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8371 Email: fliang@lifetech.com URL:
http://fulllength.invitrogen.com"
a 134 c 191 g 86 t 27 others
                                                                              /note-"Organ: colon_ins; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Technologies, a division of Invitrogen 9800 Medical Center
               tissue mRNA and cDNA amplification were performed low stringency conditions."
189 c 173 g 131 t
                                                                                                                                                                                          /dev_stage="Adult"
                                                                                                                                                                                                                                  /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                           /clone_lib="CI0179"
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RESULT 27
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AI264358/c
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                  A1669655
A1669655.1
                                                          wc12a05.x1
similar to
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Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AI264358 636 bp mRNA linear EST 27-JAN-1999 q109f04.xl Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:1855999 3' similar to TR:042154 042154 GLUCOSE-6-PHOSPHATASE;, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Insert Length: Std Error: 0.00
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Location/Qualifiers
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National Cancer Institute, Cancer Genome Anat
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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                                                                                                                                                                                                                                                                                                                                                                                               /note-*Organ: mixed (see below); Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_1: Eor RI; Equal amounts of plasmid DNA from three normalized libraries (melanocyte 2NbHM, pregnant uterus NbHPU, and fetal heart NbHH19W) were mixed, and scircles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 260232-265223, 340488-345479, and 484488-489479.**

38 a 150 c 228 g 116 t
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pregnant uterus"
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/db_xref="taxon:9606"
/clone="IhAGE:1855999"
/clone_lib="Soares_NhHMPu_S1"
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                                                      649 bp mRNA linear EST 17-DEC-1999 NCI_CGAP_Pr28 Homo sapiens cDNA clone IMAGE:2314928 3' TR:042154 042154 GLUCOSE-6-PHOSPHATASE;, mRNA sequence.
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                                                                                           Eukaryota; Metazoa; Chordata; Cranlata; Vertebrata; F
Mammalla; Eutheria; Primates; Catarrhini; Hominidae;
1 (bases 1 to 650)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collect
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cDNA Library Preparation: M. Bento Soares, Ph.D. cDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bbo.llnl.gov/Dbrp/image/image.html
Insert_Length: 768 Std_Error: 0.00
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 649)
NCI-GGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                  Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: CGAP (Stanford)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tissue Procurement: Michael J. Brownstein, M.D., Ph Emmert-Buck, M.D., Ph.D.
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cDNA Library Preparation: Ling Hong/Rubin Laboratory
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with a modified polylinker; Plasmid DNA from the
normalized library NCI_CGAP_Pr22 was prepared, and ss
circles were made in vitro. Following HAP purification,
this DNA was used as tracer in a subtractive hybridization
reaction. The driver was PCR-amplified cDNAs from a pool
of 5,000 clones made from the same library (cloneIDs
985608-986759, 1101192-1101959, and 1217928-12206I5).
Subtraction by Bento Soares and M. Fatima Bonaldo.

a 154 c 230 g 117 t 7 others
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/clone_lib="NCI_CGAP_Pr28"
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/db_xref="taxon:9606"
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/lab_host="DH10B"
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IMAGE:5433602 5',
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Matches
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BF725110
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Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
plate: LLCM1909 row: f column: 03
                                                                                                                                                                                                                                                                                                                                                                                                                              Wistow,G.J., Bernstein,S., Behal,A. and Smith,D. NEIBANK: EST analysis and bioinformatics for ocular Invest. Ophthalmol. Vis. Sci. 41 (2000) In press
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Location/Qualifiers
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Seq primer: M13RP1 reverse primer (ABI).
Location/Qualifiers
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                                                                                                                                                                                                                                                           Email: graeme@helix.nih.gov
Plate: 12 row: c column:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone_lib="NH_MCC_100"
/clone_lib="NH_MCC_100"
/tissue_type="hepatocellular carcinoma, cell line"
/lab_host="NH10B (phage=resistant)"
/lab_host="Organ: liver; Vector: pOTB7; Site_1: XhoI; Site_2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GCCACGAG(G). Size-selected >500bp for average insert size
1.8kb .Library constructed by Ling Hong in the laboratory
of Gerald M. Rubin (University of California, Berkeley)
using ZAP-cDNA synthesis kit (Stratagene) and Superscript
II RT (Life Technologies). Note: this is a NIH_MGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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                                                                                                                                                                                                                                                                                                                                                                  Eye Institute
                      /tissue_type="Iris"
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/lab_host="EMDH10B"
                                                                                                                             /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="bx12c11"
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234 c
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/db_xref="taxon:9606"
/clone="IMAGE:5433602"
                                                                                                           /clone_lib="Human Iris cDNA (Un-normalized, unamplified):
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TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BG422683.1 GI:13329189
EST.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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/tab_host="DH10B (phage-resistant)"
/lab_host="DH10B (phage-resistant)"
/note="Organ: kidney; Vector: pOTBP; Site_1: XhoI; Site_2: Corned into EcorI/XhoI sites using the following 5' cloned into EcorI/XhoI sites using the following 5' adaptor: GCCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."
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Center (NISC)."
208 c 183 g
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/db_xref="taxon:9606"
/clone="IMAGE:4587551"
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Best Local Similarity 100.0%, From No. 46;
Best Local Similarity 100.0%, From No. 46;
Best Local Similarity 100.0%, From No. 46;
Best Commerce of Mismatches 0; Indels 0; Gaps 0;

Oy 688 tigggetgetgggecoctgg 708
Best 199 TGGGCTCCTGG 219

Search completed: June 19, 2002, 01:45:26

Job time: 2007 sec
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Maximum DB
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Copyright (c) 1993 - 2000 Compugen
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Oligonucleotide:
Human secondary:
Human secondary:
Oligonucleotide:
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ALIGNMENTS

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cDNA; 1057

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(first entry)

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This sequence encodes isolated from activate
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Matches 1056; Conser
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                                                                                                                                                                                                                                                                               WPI; 199
Antigen OX-40 is specifically expressed on the cell surface of antigen activated T-cells, especially, for example, CD4+ T-cells. A human cDNA encoding the human OX-40 homologue was cloned as follows. Using the Experimental Autoimmune Encephalomyelitis model in rats the OX-40 antigen was identified (expressed on the surface of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human Ox-40; activated multiple sclerosis; sax T-cell lymphoma; ss.
                                                                                                                                                                             Nucleic acid encoding an activated T-cell antigen, Ox-40 - used develop prods. for detection and therapy of conditions mediated activated T-cells, eg. multiple sclerosis, rheumatoid arthritis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human
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                                                                                                                                      Claim
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DB; AAR76996.
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; rheumatoid arthritis;
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Best Local :
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 idm.
                                                                                                                                                                                                                                    Stimulatory primary signalling motif; immune cell; signal transduction; chimeric receptor; inflammatory disease; autoimmune disease; asthma; eczema; congenital disease; cystic fibrosis; sickle cell anemia; dermatological disease; psoriasis; neurological disease; multiple sclerosis; transplant-related disease; metabolic disease; organ transplant rejection; graft versus host disease; organ transplant rejection; graft versus host disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               activated autoantigen-specific CD4+ T-cells present at the site of inflammation but absent on CD4+ T-cells at non-inflammatory sites) and CDNA encoding the antigen was isolated. PCR primers were designed and used to clone murine OX-40 cDNA by PCR from RNA isolated from murine CD4+ T-cells activated with concanavalin A. Then the murine OX-40 cDNA was used to probe a cDNA lambda gtll library from human activated T lymphocytes to obtain human OX-40 cDNA. The published patent application states that the OX-40 cDNA sequence is also in SQ ID no. 1, but this sequence is not present in the spec. A nucleic acid having the sequence in SQ ID no 1 and the polypeptide encoded by it are claimed.
                                                                                                                                                                                                                                                                                                                                       Oligonucleotide
                          Finney HM,
                                                                                  01-NOV-1999;
                                                                                                             01-NOV-2000;
                                                                                                                                          10-MAY-2001
                                                                                                                                                                    WO200132709-A2.
                                                                                                                                                                                                Synthetic
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                                                       (CELL-)
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                                                       CELLTECH CHIROSCIENCE
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                             Lawson ADG
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                                                                                                             2000WO-GB04183
                                                                                  99GB-0025848
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                                                                                                                                                                                                                           diabetes;
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                                                                                                                                                                                                                                                                                                                                      secondary signalling motif.
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Best Local
                                                                                                                                                                                                                                                                        Human; primary signalling motif; sequence block; SB; immunosuppressive; secondary signalling sequence; antimicrobial; anti-inflammatory; dermatological; neuroprotective; cytostatic; anti-HTV; antiasthmatic; antisickling; antipsoriatic; antidiabetic; gene therapy; diabetes; immune cell signal transduction; infection; inflammation; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           secondary signalling sequences. The specification describes stimulatory primary signalling motifs. Primary motifs are efficient at at mediating immune cell signal transduction, particularly when incorporated in an intracellular signalling domain of a chimeric receptor. The primary signalling motif can be combined in any way so as to achieve the desired level of activation (or inhibition) of a number of secondary messenger cascades. The signalling motifs are useful in therapy and in the manufacture of medicament for treating or preventing disease in humans or animals. They are are useful for treating lumman patients suffering from infectious diseases e.g. human lummondeficiency virus (HIV) infections, inflammatory/autoimmune diseases such as asthma and eczema, congenital diseases e.g. cystic fibrosis, sickle cell anemia, dermatological diseases e.g. sporiasis, neurological diseases e.g. multiple sclerosis, transplant-related disease e.g. organ
             Finney
                                                                                                                                                                                                                                           organ transplant
                                                                                                                                                                                                                                                                                                                                                                          Human
                                                                                                                                                                                                                                                                                                                                                                                                           07-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel cytoplasmic signalling protein and chimeric receptor protein, useful for treating HIV infection, asthma, eczema, psoriasis, multiple sclerosis, contain non-natural stimulatory primary signalling motif -
                                                                            01-NOV-1999;
                                                                                                             01-NOV-2000; 2000WO-GB04193
                                                                                                                                                                             WO200132867-A1
                                                                                                                                                                                                                                                          immune cell signal transduction; infect
autoimmune disease; congenital disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                           AAH24477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAH24477 standard; DNA; 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 117
                                            (CELL-) CELLTECH CHIROSCIENCE
                                                                                                                                             10-MAY-2001
                                                                                                                                                                                                              Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 transplant rejection, graft versus host disease, metabolic/idiopathic disease e.g. diabetes, and cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Oligonucleotides AAH24886-87 were used to construct DNA encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 2;
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                                                                                                                                                                                                                                                                                                                                                                          secondary signalling
             MH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      83;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fig 3; 45pp; English.
             Lawson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
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                                                                            99GB-0025853
                                                                                                                                                                                                                                            rejection;
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                                                                                                                                                                                                                                                                                                                                                                          motif SB34 oligo F1340A.
                                                                                                                                                                                                                                              SS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 83;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ç;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11 T; 0 other
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2.3
                                                                                                                                                                                                                                                            psoriasis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .3e-27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sclerosis), organ transplant rejection of sclerosis), organ transplant rejection of sclerosis), organ transplant rejection of cancer). The metabolic/idiopathic diseases (e.g. diabetes or cancer). The present sequence is one of a large number of oligonucleotides used in the construction of sequence blocks (SBs) of primary and secondary signalling motifs. Primary signalling motifs are sequences that transduce either a stimulatory or an inhibitory signal, which regulates primary activation of the T cell receptor (TCR) complex. Secondary motifs impart secondary or co-stimulatory signalling capacity to a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           these primary signalling motifs are useful in medicine and research. They are useful in therapy, or in the manufacture of a medicament for treating or preventing disease in humans or in animals. These diseases include infections (e.g. HIV (human immunodeficiency virus) infection), inflammatory or autoimmune diseases (e.g. asthma or eczema), congenital diseases (e.g. systic fibrosis or sickle cell anaemia), dermatological diseases (e.g. psoriasis), neurological diseases (e.g. multiple sclerosis), organ transplant rejection or graft-versus host disease, or matabolic disease, or disbette or cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New nucleic acids encoding polypeptides with expanded primary signaling motifs, for use in gene therapy, particularly for treating or preventing infections, inflammations or autoimmune diseases in humans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        a consensus amino acid sequence. These motifs are extremely efficient at mediating immune cell signal transduction, particularly when incorporated into an intracellular signalling domain of a chime receptor. Nucleic acids that encode, and polypeptides that contain,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI;
                                                                                                                                                        neurological disease; organ transplant rejection; diabetes; ca
graft-versus-host disease; adaptor receptor protein; sequence
SB; primary signalling motif; secondary signalling motif; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The
                  01-NOV-2000; 2000WO-GB04189
                                                     10-MAY-2001.
                                                                                                                                                                                                              autoimmune disease; cystic fibrosis; sickle cell anaemia; psoriasis;
                                                                                                                                                                                                                                antisickling; antipsoriatic; neuroprotective; immunosuppressive;
antidiabetic; cytostatic; HIV infection; inflammation;
                                                                                                                                                                                                                                                                    Human; anti-HIV; antiinflammatory; antiasthmatic; dermatological;
                                                                                                                                                                                                                                                                                                   Human secondary signalling
                                                                                                                                                                                                                                                                                                                                         08-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                               AAH24543 standard; DNA; 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            acccccatccaagaggagcaggc 817
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cggagggaccagaggctgcccccgatgcccacaagccccctgggggaggcagtttccgg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       83;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                     (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     relates
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3; 43pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                to novel primary signalling motifs containing d sequence. These motifs are extremely
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   . 88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ç
                                                                                                                                                                                                                                                                                                       motif SB34 oligo F1340A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 83;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      36 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      T; 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 22;
2.3e-27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 117;
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CC receptor protein comprising an extracellular ligand-binding domain, a ctransmembrane domain and an intracellular signalling domain. The contracellular signalling domain and cintracellular signalling domain. The cintracellular signalling domain comprises the cytoplasmic portion of at least one adaptor protein, and the extracellular ligand-binding domain comprises the cytoplasmic portion of at cleast one adaptor protein, and the extracellular ligand-binding domain comprises the cytoplasmic portion of at least one adaptor protein, and the manufacture of a medicament for the creatment or receptor protein and the nucleic acid encoding it are useful in therapy. They are useful in the manufacture of a medicament for the creatment or prevention of diseases in humans and animals. They are useful in the treatment of infectious diseases (e.g. HIV infection), compenital diseases (e.g. cystic fibrosis and sickle cell anaemia), compenital diseases (e.g. cystic fibrosis and sickle cell anaemia), compenital diseases (e.g. psoriasis), neurological diseases (e.g. transplant rejection, graft-versus-host compenital diseases (e.g. psoriasis), neurological diseases (e.g. transplant rejection, graft-versus-host compens sequence is one of a large number of oligonucleotides used in the construction of sequence blocks (SBs) of primary and secondary signalling motifs transduce either a stimulatory or on inhibitory signal, which regulates primary activation of the T cell receptor (TCR) complex. Secondary signalling motifs impart cemponents of the adaptor receptor protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel polynucleotide encoding adaptor receptor protein useful for treating human immunodeficiency virus (HIV) infection, asthma, cy fibrosis, multiple sclerosis, organ transplant rejection, diabete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cancer
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Sequence 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (CELL-) CELLTECH CHIROSCIENCE LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fig
  B₽;
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  25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          52pp;
<u>.</u>
45 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               English.
36 G;
  11 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    diabetes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cystic
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Query Match Best Local Matches 735 cggagggaccagaggctgcccccgatgcccacaagcccctgggggaggcagtttccgg 83; Similarity Conservative 100.0%; 7.8%; Score 83; DB; Pred. No. 2.3 0; DB 22; .3e-27; 0; Length 117; 0 Gaps 0

795 66 σ acccccatccaagaggagcaggc acccccatccaagaggagcaggc 817 cggagggaccagaggctgccccccgatgcccacaagccccctgggggaggcagtttccgg 88 65

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AAH24887; AAH24887 standard; DNA; 117

Oligonucleotide 22-AUG-2001 (first entry) for a secondary signalling motif.

RESULT 7
AAH24887/C
ID AAH248
XX
AC AAH248
XX
DT 22-AUG
DT 22-AUG
XX
Chimon
XX
KW Chimen
KW Chimen
KW dermat
KW dermat
KW dermat
KW organ
KW idiopa dermatological disease; psoriasis; neurological disease; multiple sclerosis; transplant-related disease; metabolic organ transplant rejection; graft versus host disease; Stimulatory primary signalling motif; immune cell; signal transduction; chimeric receptor; inflammatory disease; autoimmune disease; asthma; eczema; congenital disease; cystic fibrosis; sickle cell anemia; idiopathic disease; diabetes; cancer;

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RESULT 8
AAH24478/C
ID AAH244
XX AH244
XX O7-AUG
DT 07-AUG
DE Human
XX Human;
KW Secon(
KW Secon(
KW dermat
KW antis:
KW antis:
KW autoir
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Best Local S
Matches 78
                secondary signalling sequence; antimicrobial; antiinflammatory; dermatological; neuroprotective; cytostatic; anti-HTV; antiasthmatic; antisickling; antipsoriatic; antidiabetic; gene therapy; diabetes; immune cell signal transduction; infection; inflammation; cancer; autoimmune disease; congenital disease; psoriasis; neurological disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      mediating immune cell signal transduction, particularly when incorporated in an intracellular signalling domain of a chimeric receptor. The primary signalling motif can be combined in any way so as to achieve the desired level of activation (or inhibition) of a number of secondary messenger cascades. The signalling motifs are useful in therapy and in the manufacture of medicament for treating or preventing disease in humans or animals. They are are useful for treating human patients suffering from infectious diseases e.g. human immunodeficiency virus (HIV) infections, inflammatory/autoimmune diseases such as another adverse the secondary of the seases of contents of the seases of contents of the seases of contents of the seases and contents of the seases and contents of the seases are contents.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    such as asthma and eczema, congenital diseases e.g. cystic fibrosis, sickle cell anemia, dermatological diseases e.g. psoriasis, neurological diseases e.g. multiple sclerosis, transplant-related disease e.g. organ transplant rejection, graft versus host disease, metabolic/idiopathic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  secondary signalling sequences. The specification describes stimulatory primary signalling motifs. Primary motifs are efficient at at mediating immune cell signal transduction.
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                                                                                                                                          Human secondary signalling motif SB34 oligo F1340B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 2; Fig 3; 45pp; English.
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                                                                                                          Human;
                                                                                                                                                                                                                                                      AAH24478
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                                                                                                                                                                                                                                                                                                                                                                                                                                              768
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                                                                                                                                                                                                                                                                                                                                                                                                           aagccccctgggggaggcagtttccggacccccatccaagaggagcaggccgacgcccac
                                                                                                                                                                                                                                                                                                                                                             tccaccctggccaagatc 845
                                                                                                                                                                                                                                                                                                                                           TCCACCCTGGCCAAGATC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cytoplasmic signalling protein and chimeric receptor protein, l for treating HIV infection, asthma, eczema, psoriasis, multi
 transplant
                                                                                                          primary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18; Conservative
                                                                                                                                                                                                                                                    standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        treating HIV infection, asthma, eczema, psoriasis, multiple contain non-natural stimulatory primary signalling motif -
                                                                                                                                                                                (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BP; 11 A;
                                                                                                          signalling motif; sequence block; SB;
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   rejection;
                                                                                                                                                                                                                                                    DNA;
                                                                                                                                                                             entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        35 C;
                                                                                                                                                                                                                                                      117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 78; DB; Pred. No. 4e-
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        45 G;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            78;
No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 22;
4e-25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0
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                                                                                                          immunosuppressive;
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                    disease
                                                                                                                                                                                                                                                                                                                                                                                                                                              827
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when incorporated into an intracellular signalling domain of a chimeric receptor. Nucleic acids that encode, and polypeptides that contain, these primary signalling motifs are useful in medicine and research. They are useful in therapy, or in the manufacture of a medicament for ctreating or preventing disease in humans or in animals. These diseases include infections (e.g. HIV (human immunodeficiency virus) infection), contifiammatory or autoimmune diseases (e.g. asthma or eczema), congenital diseases (e.g. psoriasis), neurological diseases (e.g. psoriasis), neurological diseases (e.g. multiple ctreation), organ transplant rejection or graft-versus-host disease, or metabolic/diopathic diseases (e.g. diabetes or cancer). The present sequence is one of a large number of oligonucleotides used in the construction of sequence blocks (SBs) of primary and secondary csignalling motifs. Primary signalling motifs are sequences that ctransduce either a stimulatory or an inhibitory signal, which regulates or motifs impart secondary or co-stimulatory signalling capacity to a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New nucleic acids encoding polypeptides with expanded primary signaling motifs, for use in gene therapy, particularly for treating or preventing infections, inflammations or autoimmune diseases in humans
                                                                                                                                                                                                                                                                                                                                                         The invention relates to novel primary signalling motifs containing a consensus amino acid sequence. These motifs are extremely efficient at mediating immune cell signal transduction, particularly
Sequence 117
                                                                                                                                                                                                                                                                                                                                                                                                                                  Example
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Finney HM, Lawson ADG;
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                                     molecule
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 BP;
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AAH24544/c
ID AAH245
XX
AC AAH245
XX
DT 08-AUG
XX
DE Human
XX
Human;
                                                                                                                                               Matches
                                                                                                                                                            Query Match
                                                       AAH24544 standard; DNA; 117
                                                                                                       828
                                                                                                                                 768
                                                                                                                    83
                                                                                                                                                     Local
                                                                                          23
                                                                    9
                                                                                                                   TCCACCCTGGCCAAGATC
                                                                                                      tccaccctggccaagatc
                                                                                                                                                      Similarity
                                                                                                                                               Conservative
                                                                                                                                                     100.0%;
                                                                                                       845
                                                       ВP
                                                                                                                                               0;
                                                                                                                                                      Score 78;
Pred. No.
                                                                                                                                               Mismatches
                                                                                                                                                            78;
                                                                                                                                                      4e-25;
                                                                                                                                                            DB
                                                                                                                                               0,
                                                                                                                                                            Length 117;
                                                                                                                                               Indels
                                                                                                                                               0;
                                                                                                                                               Gaps
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0;

Human; anti-HIV; antiinflammatory; antiasthmatic; dermatological;

signalling motif SB34 oligo F1340B

Human secondary

08-AUG-2001 AAH24544;

(first entry)

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RESULT 1
AAT00826
ID AATC
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                                                                                                                                     QY
                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                  inflammatory and autoimmune diseases (e.g. asthma and eczema), depending the diseases (e.g. cystic fibrosis and sickle cell anaemia), dermatological diseases (e.g. psoriasis), neurological diseases (e.g.) multiple sclerosis), organ transplant rejection, graft-versus-host disease and metabolic/idiopathic diseases such as diabetes and cancer. The present sequence is one of a large number of oligonucleotides used in the construction of sequence blocks (SBs) of primary and secondary signalling motifs transduce either a stimulatory or an inhibitory signal, which regulates primary activation of the T cell receptor (TCR) complex. Secondary signalling motifs may be used as components of the adaptor receptor protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        neurological disease; organ transplant rejection; diabetes; cancer; graft-versus-host disease; adaptor receptor protein; sequence block; SB; primary signalling motif; secondary signalling motif; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               antisickling; antipsoriatic; neuroprotective; immunosuppressive; antidiabetic; cytostatic; HIV infection; inflammation; autoimmune disease; cystic fibrosis; sickle cell anaemia; psoria neurological disease; organ transplant rejection; diabetes; canc
                                                                                                                                                                                                                                                                                                                                                                                                                     is not CD8 or a major histocompatibility complex (MHC) class I protein. The adaptor receptor protein and the nucleic acid encoding it are useful in therapy. They are useful in the manufacture of a medicament for the treatment or prevention of disease in humans and animals. They are useful in the treatment of infectious diseases (e.g. HIV infection),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to a novel nucleic acid encoding an adaptor receptor protein comprising an extracellular ligand-binding domain, a transmembrane domain and an intracellular signalling domain. The intracellular signalling domain comprises the cytoplasmic portion of at least one adaptor protein, and the extracellular ligand-binding domain
AAT00826 standard; cDNA to mRNA;
                                                                                                                                                                                                                               Sequence 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 3; Fig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   fibrosis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Finney HM, Lawson ADG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (CELL-) CELLTECH CHIROSCIENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200132866-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                        828
                                                                                                                 83
                                                                23
                                                                                                                                                                            Local
                           10
                                                                                                                             aagccccctgggggaggcagtttccggacccccatccaagaggagcaggccgacgcccac 827
                                                                             tccaccctggccaagatc 845
                                                                                                                AAGCCCCCTGGGGGAGGCAGTTTCCGGACCCCCATCCAAGAGGAGCAGGCCGACGCCCAC
                                                                 TCCACCCTGGCCAAGATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2001-328790/34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                polynucleotide encoding adaptor receptor protein useful for ing human immunodeficiency virus (HIV) infection, asthma, cysis, multiple sclerosis, organ transplant rejection, diabetes
                                                                                                                                                                  Similarity
78; Conser
                                                                                                                                                                  Conservative
                                                                                                                                                                                                                               BP; 11 A; 35 C; 45 G;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               52pp; English.
                                                                                                                                                             100.08; **
                                                                σ
                                                                                                                                                                           Score 78;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LID
                                                                                                                                                                 Mismatches
  618
                                                                                                                                                                                                                               26 T; 0 other;
                                                                                                                                                                            DB 22;
4e-25;
                                                                                                                                                                  0
                                                                                                                                                                                       Length 117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   thma, cystic diabetes and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               psoriasis;
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ID AAV3
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                                                                                                                                                                                                                                                                                           RESULT
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Best Local S
Matches 28
                                                                                     Key
                                                                                                                          Mus sp.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10-OCT-1995
 21-JUL-1998
                                                                                                                                                                                                                                          AAV32640;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAT00826;
                                                                                                                                                                                                                                                                                                                                  404
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glycoprotein cells.
                                                                                                                                                 OX40; cytokine; T cell antigen; TH-2 immune response; OX40-L; OX40/Fc; ss.
                                                                                                                                                                                                                                                                                           AAV32640 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New isolated DNA encoding the OX40 ligand polypeptide and host cells, used to produce recombinant ligand used prim. T cell culture, to modulate immune response etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US5457035-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 membrane glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OX40; OX40-L;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30-MAR-1996
US5783665-A
                                                                                                                                                                                               Mouse OX40 extracellular domain encoding cDNA
                                                                                                                                                                                                                                25-SEP-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This sequence encodes the extracellular of the cD4 positive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (IMMV ) IMMUNEX CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23-JUL-1993;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                      424 acaaccaggcctgcaagccctggaccaa 451
                                                                                                                                                                                                                                                                                                                                                                         acaaccaggcctgcaagccctggaccaa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1995-357992/46
DB; AAR81881.
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28; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fanslow WC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Column
                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cytokine; cell surface molecule;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            93US-0097827
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           93US-0097827
                           /*tag= a
/product= "Mouse OX40 extracellular region"
/note= "CDS does not contain a stop codon"
                                                                        Location/Qualifiers
1..618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               148
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                                                                                                                                                                                                                                                                                           cDNA to mRNA; 618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Α;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 28; DB; Pred. No. 0.0 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               151 G;
                                                                                                                                                                                                                                                                                                                                                                         431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Goodwin
                                                                                                                                                                                                                                                                                           ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               132 T; 0 other
                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 16;
0.0079;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          domain of OX40, a membrane subset of activated T
                                                                                                                                                                                                                                                                                                                                                                                                                                      0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 618;
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RESULT 1
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present sequence represents the mouse OX40 extracellular domain encoding cDNA. The extracellular domain of OX40 is its ligand binding domain. The present cDNA was used in the construction of the chimeric OX40/Fc cDNA (AAV32640). The invention claims for a murine OX40-L cytokine (AAW48975) that binds to the OX40 murine T cell antigen. The OX40-L protein is claimed to be useful for co-stimulation of T-cell production and in binding assays for detecting OX40 or its homologues. The OX40-L protein is also claimed to generate a TH-2
WPI; 1995-357992/46.
P-PSDB; AAR81882.
                                                                                                                                                                                                                                                                                                                                           CDS
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                                                                                                                                                                                                                                                                                                                                                                                                  Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0X40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Plasmid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 1; Col 31-32; 26pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Purified polypeptide OX-40 ligands - production and binding assays for OX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Baum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (IMMV ) IMMUNEX CORP
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22-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22-JUN-1995;
                                                                                                         ( VMMI)
                                                                                                                                                  23-JUL-1993;
                                                                                                                                                                                           23-JUL-1993;
                                                                                                                                                                                                                                     10-OCT-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                pDC406/0X40,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30-MAR-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAT00829
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          424 acaaccaggcctgcaagccctggaccaa 451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   acaaccaggcctgcaagccctggaccaa 431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1998-427099/36.
                                                                                                                                                                                                                                                                                                                                                                                                                                         OX40-L; cytokine; cell surface molecule; plasmid; 5/OX40/Fc*; membrane glycoprotein; ss.
                                                                                                         IMMUNEX CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PDC406/0X40/Fc*
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                                                                  Fanslow WC,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first
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95US-0494574.
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                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
1..1317
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     `>
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                                                                  Gayle
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Pred.
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                                                                  RВ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gands - for for ox-40 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       151
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                                                                  Goodwin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          co:stimulation of T-cell and homologues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      в 19;
.0079;
                                                                    RG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RG;
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Best Local :
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and
                                                                                                                                                                                                                                                                                                                                            used to transform the CV-1/EBNA (ATCC CRL 10478) monkey kidney cel line. Culture supernatant was purified by affinity chromatography and this was used, together with labeled goat anti-human IgG to
                                                                                                                                                                                                                                                                                                                                                                                   This plasmid encodes an OX40/Fc antibody fragment mutein protein and is used to express a soluble OX40/Fc mutein fusion protein use in detecting cDNA clones encoding a OX40 ligand. The Fc fragment may be derived from human IgG1, and the plasmid may be
chimeric;
         OX40/Fc; cytokine;
                                     OX40/FC CDNA.
                                                              25-SEP-1998
                                                                                         AAV32636;
                                                                                                                  AAV32636 standard;
                                                                                                                                                                                                                                                                                                     Sequence 1317
                                                                                                                                                                                                                                                                                                                                 screen various cell lines
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 2; Column 35-38; 26pp; English.
                                                                                                                                                                                               424 acaaccaggcctgcaagccctggaccaa 451
                                                                                                                                                                                  404 acaaccaggcctgcaagccctggaccaa 431
                                                                                                                                             13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             isolated DNA encoding the OX40 ligand polypeptide - host cells, used to produce recombinant ligand used \mathfrak n. T cell culture, to modulate immune response etc.
                                                                                                                                                                                                                                                    Similarity
 SS
                                                                                                                                                                                                                                       Conservative
                                                                (first
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                                                                                                                  CDNA
            н
                                                                entry)
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            cell antigen;
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pred. No.
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                                                                                                                   1317
            TH-2 immune response; OX40-L;
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Synthetic.
Chimeric -
22-JUN-1995;
         21-JUL-1998.
                   US5783665-A
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                                                                                                                                              Chimeric -
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95US-0494574
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673..675
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/note= "encodes
619..1314
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mutant"
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mutant"
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         fusion protein that contains the extracellular domain of mouse OX40 fused to the mutated Fc region of the human IgGl antibody. The fusion protein was used for detecting cDNA clones encoding an OX40 ligand. The invention claims for a murine OX40-L cytokine (AAW4897 that binds to the murine T cell antigen, OX40. The OX40-L protein is claimed to be useful for co-stimulation of T-cell production and in binding assays for detecting OX40 or its homologues. The OX40-L protein is also claimed to generate a TH-2 immune response.
                                                                                                               (WEIN/)
                            Nucleic acid encoding an activated T-cell antigen, Ox-40 -develop prods. for detection and therapy of conditions mediactivated T-cells, eg. multiple sclerosis, rheumatoid arthr
                                                                       WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI;
           Example;
                                                                                          Vandenbark AA,
                                                                                                                                             04-FEB-1994;
                                                                                                                                                                06-FEB-1995;
                                                                                                                                                                                    10-AUG-1995
                                                                                                                                                                                                        WO9521251-A
                                                                                                                                                                                                                            Synthetic
                                                                                                                                                                                                                                                Primer; human
                                                                                                                                                                                                                                                                  PCR primer 1
                                                                                                                                                                                                                                                                                        21-DEC-1995
                                                                                                                                                                                                                                                                                                            AAQ93255;
                                                                                                                                                                                                                                                                                                                              AAQ93255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1317 BP; 322 A; 417 C; 337 G;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     production and
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22-JUN-1995;
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CANTAB PHARM RES
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          Page
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  polypeptide Ox-40 ligon and binding assays
                                                                                                                                                                                                                                                                                                                               standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fanslow WC,
                                                                                                                                                                                                                                                                                                                                                                                                                        2.6%;
ilarity 100.0%;
Conservative
                                                                                                                                                                                                                                                                   for human OX-40 cDNA.
                                                                                                                                                                                                                                                                                     (first
          50;
                                                                                                                                                                                                                                                OX-40; PCR; SS
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95US-0494574.
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                                                                                           Weinberg
                                                                                                                                                                                                                                                                                     entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OX-40 ligands -
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                                                                                                                                                                                                                                                                                                                               В₽
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                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                     451
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I. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          241 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 19;
0.0074;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   r co:stimulation and homologues
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 1317;
                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                             x-40 - used this mediated heretarities,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (AAW48975)
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RESULT 1
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Best Local S
Matches 24
      The invention relates to a nucleic acid comprising a sequence of 18 bases, of a segment of chemically pretreated DNA (CP DNA) e.g. with bisulphite, of genes associated with tumour suppression and oncogenes having a sequence taken from 536 (actually 533 since numbers 408, 458 and 500 are missing from the sequence listing) sequen (Ss) and sequences complementary to (Ss). The nucleic acid may be a peptide nucleic acid-oligomer (PNA) of at least 9 nucleotides and may form part of a set of probes for detecting the cytosine methylation st and/or single nucleotide polymorphisms and also to be used in an array for analysing diseases associated with Cpc dinucleotides e.g. cancers and tumours. The probes can also be used in a method for
                                                                                                                                                                                                                                                                                                                                      06-APR-2000;
07-APR-2000;
30-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Antigen OX-40 is specifically expressed on the cell surface of antigen activated T-cells, especially, for example, CD4+ T-cells. A human cDNA encoding the human OX-40 homologue was cloned using primers 1 and 2. Template DNA for PCR amplification to product the human OX-40 cDNA can be extracted from the lambda GT11 cDNA library from human activated T-lymphocytes produced by Clontech, Palo Alto, California (Catalog No. HL10316).
                                                                                                                                                                                                                                                  WPI;
                                                                                                                                                                                        analysing -
                                                                                                                                                             Claim
                                                                                                                                                                                                               genes
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cytosine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; tumour suppressor gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tumour suppressor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18-DEC-2001
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                                                                                                                                                                                                                         Fragments
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24; Conservative
                                                                                                                                                                                                                                                                                                   EPIGENOMICS
                                                                                                                                                             SEQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                standard;
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                                                                                                                                                                                                                                                                           Piepenbrock
                                                                                                                                                                                            of chemically modified genes associated with tumour suppressor oncogenes, useful in designing primers and probes for diseases associated with cytosine methylation state e.g.
                                                                                                                                                                                                                                                                                                                        ; 2000DE-1013847.
; 2000DE-1019058.
; 2000DE-1019173.
; 2000DE-1032529.
; 2000DE-1043826.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                             ID No
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gene derived
                                                                                                                                                             307;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA;
                                                                                                                                                                                                                                                                                                   AG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                dinucleotide;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ds.
                                                                                                                                                            27pp; English.
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Pred.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              oncogene; antitumour;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    chemically modified
                                                                                                                                                                                                                                                                          Χ.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                single-nucleotide polymorphism;
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genetic

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RESULT 1
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Best Local :
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13-APR-2000;
31-OCT-2000;
The present invention describes differentially expressed general in anglogenesis (I), and the polypeptides that encode them. cardiovascular activity, and can be used in the modulation of anglogenesis. The nucleic acids and polypeptides may be used prevention, diagnosis and treatment of diseases associated with the presentation of the presentati
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           angiogenic disorder; wound healing; cancer; cardiovascular; psoriasis;
vascular tumour; proliferative tumour; proliferative vitreoretinopathy;
rheumatoid arthritis; Crohn's disease; atherosclerosis; endometriosis;
neovascularisation; restenosis; hypertension; aneurysm; angina;
myocardial infarction; chronic heart condition; osteoporosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          and/or therapy of existing diseases or the predisposition to specific diseases, by analysing cytosine methylations. The parameters may be compared to another set of genetic and/or epigenetic parameters, the differences serving as basis for diagnosis and/or prognosis events whi are disadvantageous to patients. The present sequence is one of the 533 genomic sequences derived from tumour suppressor genes and
                                                                                                                                       Example
                                                                                                                                                                                                    Differentially expressed genes involved in angiogenesis, useful treating e.g. vascular tumors, atherosclerosis and/or restenosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-2000; 2000WO-US30051
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OX40 reverse
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200132926-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PCR primer; hybridisation; probe;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAH22273;
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                                                                                                                                                                                                                                                                                                                                                                     (GETH
                                                                                                                                                                                                                                                                                                                                                                                          (CURA-)
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                                                                                                                                          19;
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23; Conservative
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; 2000US-0196802.
; 2000US-0703350.
                                                                                                                                     Page 147;
                                                                                                                                                                                                                                                                                                                       Gerritsen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PCR primer SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2.2%;
                                                                                                                                  182pp; English.
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                                                                   (I) have
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       antagonists may also be used to down regulate expression and activity
and modulate angiogenesis. The antibodies may also be used as diagnostic
agents for detecting the presence of the polypeptides in samples.

Disorders that may be prevented, diagnosed and/or treated by the above methods include, for example vascular tunours, proliferative tumours, attended to the state of the sample vascular timours, proliferative tumours, proliferative tumours, proliferative tumours, attended to the state of the sample vasculation, provided arthritis, Crohn's disease, and associated with neovascularisation, restenosis subsequent to balloon angioplasty, scar tissue over production, peripheral vascular disease, typertension, inflammatory vasculatides, Reynaud's disease and Reynaud's phenomenon, aneurysms, arterial restenosis, thrombophlebitis, lymphangitis, lymphedema, wound healing and tissue repair, ischaemia creperfusion injury, angina, myocardial infarctions, chronic heart failure such as congestive heart failure, age-related macular degeneration and osteoporosis. AH22325 to AH23325 and AH898322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local S
Matches 22
                                                                                                                                                         01-NOV-1999;
13-APR-2000;
31-OCT-2000;
Differentially expressed genes treating e.g. vascular tumors,
                                                                                                                                                                                                                                                                                                                                                                                                  vascular tumour; proliferative tumour; proliferative vitreoretinopa; rheumatoid arthritis; Crohn's disease; atherosclerosis; endometrios: neovascularisation; restenosis; hypertension; aneurysm; angina;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                inappropriate angiogenesis. The polypeptides may also be use in the production of antibodies against them and in assays to modulators of their expression and activity. The antibodies antagonists may also be used to down regulate expression and
                                                                                                                                                                                                                                                                                        WO200132926-A2
                                                                                                                                                                                                                                                                                                                        Homo sapiens.
Synthetic.
                                                                                                                                                                                                                                                                                                                                                                     myocardial infarction; chr
PCR primer; hybridisation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OX40 forward PCR primer SEQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cular degeneration and osteoporosis. AAB98325 represent sequence used in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GCTTACGTATGCCATGCATACC
                                               2001-291056/30
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22; Conserv
                                                                                                             GENENTECH INC
                                                                                                                           CURAGEN CORP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  disorder;
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; 2000US-0196802.
; 2000US-0703350.
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on; chronic heart
sation; probe; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           entry)
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Pred. No
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 involved in angiogenesis, useful atherosclerosis and/or restenosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                               gene; angiogenesis; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                 cancer;
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                                                                                                                                                                                                                                                                                                                                                                                   condition;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 cardiovascular;
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                                                                                                                                                                                                                                                                                                                                                                                     osteoporosis;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  psoriasis;
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                for
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subsequent to balloon angioplasty

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RESULT 1
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ID AAA8
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AX Huma
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CC antagonists may also be used to down regulate expression and activity capents for detecting the presence of the polypeptides in samples. CC agents for detecting the presence of the polypeptides in samples. CC Disorders that may be prevented, diagnosed and/or treated by the above cc methods include, for example vascular tumours, proliferative tumours, crohn's disease, cc proliferative vitreoretinopathy, rheumatoid arthritis, Crohn's disease, cc atherosclerosis, ovarian hyperstimulation, psoriasis, endometriosis cc associated with neovascularisation, restenosis subsequent to balloon cangioplasty, scar tissue over production, peripheral vascular disease, chypertension, inflammatory vasculitides, Reynaud's disease and cc reperfusion injury, angina, myocardial infarctions, chronic heart cc conditions, heart failure such as congestive heart failure, age-related cc macular degeneration and osteoporosis. AAH22255 to AAH22325 and AAB98322 cc to AAB98325 represent sequence used in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     angiogenesis. The nucleic acids and polypeptides may be used in the prevention, diagnosis and treatment of diseases associated with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention describes differentially expressed genes involved in angiogenesis (I), and the polypeptides that encode them. (I) have cardiovascular activity, and can be used in the modulation of
                                                                                                                                                                                                                                                                                                                                                                                                                                           gene therapy; vaccine; chemotaxis-modulator; angiogenesis-modulator;
cancer; immune system disorder; hyperproliferative disorder; infection;
cardiovascular disorder; neurological disease; wound healing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       antiinflammatory; cardiant; vulnerary; antiulcer; anticonvulsant;
antiparkinsonian; neuroprotective; antiviral; antibacterial; cytostatic;
antiparasitic; thrombolytic; anticoagulant; antiarteriosclerotic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     04-DEC-2000
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                                                                                                19-JAN-1999;
                                                                                                                                                           18-JAN-2000; 2000WO-US00903
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                             (HUMA-) HUMAN GENOME SCI INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       secreted protein; immunosuppressive; immunostimulant; nootropic;
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                                                                                                99US-0116330
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14;
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antiarteriosclerotic and cytostatic. The secreted proteins and their polynucleotides can be used in gene therapy and as vaccines, chemotaxis-modulators and anglogenesis-modulators. The human secreted proteins and polynucleotides can be used for diagnosing (the susceptibility to) a pathological condition by determining the presence or absence of a mutation in the polynucleotide or determining the presence or amount of expression of the protein. The polynucleotides and proteins can also be used in the treatment and diagnosis of cancer,
                                                       diseases of the immune system, hyperproliferative disorders, cardiovascular disorders and neurological disease. They can also be used to promote wound healing and to fight infection. AAA87657 to AAA87665 at AAB25664 represent sequences used in the exemplification of the present
                                                                                                                                                                                                                                                                                                                                 proteins have activities based on the tissues and cells the genes are expressed in Examples of activities include: immunosuppressive; immunostimulant; antiinflammatory; cardiant; vulnerary; antiulcer; nootropic; antiviral; anticonvulsant; antiparkinsonian; neuroprotective;
                                                                                                                                                                                                                                                                                                                                                                                                                   The polynucleotide sequences given in AAA87666 to AAA87708 encodes the human secreted proteins given in AAB25665 to AAB25755. Human secreted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             preventing, treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New isolated polynucleotide encoding preventing, treating or ameliorating
                                                                                                                                                                                                                                                                                                                antibacterial; antiparasitic; thrombolytic; anticoagulant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Komatsoulis G,
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CE;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 secreted protein useful for medical condition -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'n
                                                                                                                                                                   The polynucleotides and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Moore PA;
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RESULT 19 AAC76846 Best Loc Matches Human ORFX ORF2401 polynucleotide sequence SEQ ID NO:4801. 08-FEB-2001 AAC76846; AAC76846 standard; cDNA; 1447 BP 638 tggggctgctgggccccctgg 658 688 tggggctgctggggccccctgg 708 Local Similarity Conservative (first entry) 100.0%; F Score 21; pred. No. Mismatches v O DB 10; 21; 0; Length 1153; 0; Gaps 0

밁 Q

Sequence 1153 BP;

241 A;

376 C;

279

G;

255

T; 2

Human; open reading frame; ORFX; detection; cytostatic; hepatotropic; vulnerary; antipsoriatic; antiparkinsonian; nootropic; neuroprotective; anticonvulsant; osteopathic; antiarthritic; immunosuppressant; cardiant; immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic; hypotensive; dermatological; immunosuppressive; antiinflammatory; antiviral; antibacterial; antifungal; antirheumatic; antithyroid; antityroid; antianaemic; gene therapy; cancer; proliferative disorder; hypertension neurodegenerative disorder; osteoarthritis; graft vs host disease; cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS; cholesterol ester storage; systemic lupus erythematosus; infection; severe combined immunodeficiency; malaria; autoimmune disorder; asthma; allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound; thrombosis; damage; cartilage damage; contraceptive; hypertension

Homo sapiens

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AAK52633
ID AAK5
XX
AC AAK5
XX
DT 06-P
XX
Huma
XX
Huma
KW Huma
KW VaCo
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                                                                                                                                                                                                                RESULT
                                                                                                                                                                                                                                                                                                                                                                                              cc which represent the human OFFX open reading frames I to 3161. The OFFX CS sequences have activities such as: cytostatic; hepatotropic; vulnerary; cc antiporiatic; anticonvulsant; antiarthritic; immunosuppressant; cc immunostimulant; cardiant; thrombolytic; coagulant; vasotropic; cc antidiabetic; hypotensive; dermatological; immunosuppressant; cc antidiabetic; hypotensive; dermatological; immunosuppressive; cc antitinflammatory; antibacterial; antiviral; antifungal; antirheumatic; cc antithyroid; and antianaemic. The sequences can be used for determining ct the presence of or predisposition to, or preventing or treating ct the presence of or predisposition to, or preventing or treating creative acids can be used to express OFFX proteins in gene therapy cectors. The proteins and nucleic acids may be used to treat cancers, cc proliferative disorders, neurodegenerative disorders, osteoarthritis, creative hypertension, hypothyroidism, cholesterol ester storage, systemic lupus crythematosus, severe combined immunodeficiency (SCID), AIDS, viral, callergies, aplastic anaemia, burns, wounds, boacturnal haemoglobhnuria, antiinflammatory disease; to enhance coagulation; to inhibit thrombosis; and as a contraceptive.
                                                                                                                                                                                                                                                                                                         Query Match
Best Local S
Matches 21
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02-APR-1999;
05-APR-1999;
30-MAR-2000;
                                     Human; cytokine; cell proliferation; cell differentiation; gene th vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorder; arthritis; inflammation; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel nucleic acids and peptides derived from open reading useful for treating e.g. cancers, proliferative disorders, neurodegenerative disorders and cardiovascular disease -
               Homo
                                                                                                         Human
                                                                                                                                   06-NOV-2001
                                                                                                                                                            AAK52633;
                                                                                                                                                                                                                                                                                                                                                                          Sequence
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             sapiens
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                                                                                                       polynucleotide SEQ ID
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                                                                                                                                                                                                                                                                                                         h 2.0%;
Similarity 100.0%;
21; Conservative
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99US-0127636.
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2000US-0540763.
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                                                                            therapy;
                                                                                                                                                                                                                                                                                                         Gaps
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Matches 21
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27-APR-2000;
20-JUN-2000;
19-JUL-2000;
01-SEP-2000;
15-SEP-2000;
20-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to polynucleotides (AAK51456-AAK53435) and the encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopolesis regulating activity, tissue growth factor activity, immunomodulatory activity and activin/inhibin activity and may be useful in the diagnosis and/or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tang
Zhao
                    Phosphatase; PP; immune disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Note: Records for SEQ ID NO 2110 (AAK52581), (AAM80020) are omitted as the relevant pages were missing at the time of publication.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nucleic acids encoding polypeptides with cytokine-like activities, useful in diagnosis and gene therapy -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Xue
neuroprotective;
                                                                                                Human
                                                                                                                                                17-SEP-2001
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                                                                                                                                                                                                                                               AAH22958 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1461
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30-NOV-2000;
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)B; AAM79500.
                                                                                                phosphatase (PP) encoding cDNA (clone ID 1269556CB1)
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Wang D,
Yang Y,
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2000US-0560B75

2000US-0598075

2000US-0520325

2000US-0620325

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2000US-063561

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2000US-0728422
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                                                PP;
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Alzheimer's disease; Huntington's disease; human; cancer; nootropic; immunomodulatory; cytostatic; anticonvulsant; ss.
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Wang J,
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Wejhrman T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         249 A;
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, Zhang J, Ren
n T, Goodrich R;
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28-JAN-2000;
25-FEB-2000;
17-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention provides human phosphatases (PP) and polynucleotides encoding the phosphatases. The polypeptides can be expressed by standard recombinant methodology. The PP are useful for treating a disease or condition associated with decreased expression of functional phosphatases. Compositions containing agonists or antagonists of PP may be used to treat a disease associated with decreased expression or overexpression of PP, respectively. Such diseases may include Alzheimer's disease, Huntington's disease, immune disorders, and cancers. The present sequence represents a human phosphatase encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1089
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel phosphatases useful for treating diseases associated with decreased expression of functional phosphatases, e.g., Alzheime disease, Huntington's disease, immune disorders, and cancers -
                                                                                                                                             Human; cytokine; cell proliferation; cell differentiation; gene th vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorder; arthritis; inflammation; ss.
                                                                                                                                                                                                                                                   Human polynucleotide SEQ ID NO
                                                                                                                                                                                                                                                                                            06-NOV-2001
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ilarity 100.0%;
Conservative
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2000US-0178988.
2000US-0184959.
2000US-0190142.
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                                                                                                                                                                                                        gene therapy;
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RESULT 23
AALJ6023/C
ID AALJ60
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AAC AALJ60
XX
DT 08-JAN
DT UM-JAN
DE Human
XX
Cytost
KW Cytost
KW antial
KW vulner
KW reardia
KW reardia
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New cardia
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PN WO2001
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                                                                                                                                             Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral; antiallergic; hepatotropic; antidiabetic; antiinfamatory; antilucer; vulnerary; antiparastic; antibacterial; antifungal; antiparastic; cardiant; gene therapy; cancer; immune disorder; cardiovascular disord
                                                                                                                       cardiant; gene therapy; cancer; i
neurological disease; infection;
                                                                                                      musculoskeletal
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                                                               Homo sapiens
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musculoskeletal system related polynucleotide SEQ ID

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protein;

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standard;

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Query Match
Best Local S
Matches 21
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27-APR-2000;
20-JUN-2000;
19-JUL-2000;
01-SEP-2000;
15-SEP-2000;
20-OCT-2000;
30-NOV-2000;
                                                                                                                                                        The invention relates to polynucleotides (AAK51456-AAK53435) and the encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopoiesis regulating activity tissue growth factor activity, immunomodulatory activity and activin/inhibin activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and
 1178
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Zhao
                                                                                                                                                                                                                                                                               Claim 1;
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                                                                                                                                                                                                                                                                                                   Nucleic acids useful in diag
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                                                                                              Sequence 1658
                                                                                                                 Note: Records for SEQ ID NO 2110 (AAK52581), (AAM80020) are omitted as the relevant pages were missing at the time of publication.
                                                                                                                                                   inflammation.
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          tggggctgctgggccccctgg
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DB; AAM78516.
tggggctgctgggccccctgg
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                                                                                                                                                                                                                                                                               Page 981-983;
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Wang D,
Yang Y,
                                                                                                                                                                                                                                                                                                  cids encoding polypeptides with diagnosis and gene therapy -
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2000US-0560875.
2000US-0598075.
2000US-0620325.
2000US-0654936.
2000US-0663561.
2000US-0693325.
2000US-0728422.
                                          Conservative
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, Wang J, Zh
Wejhrman T,
                                                                                              282 A; 536 C;
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Zhang
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ang J, Ren
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11-JUL-2000
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2000US-0179065
2000US-0186628
2000US-0186628
2000US-0188664
2000US-019874
2000US-0198123
2000US-0198123
2000US-0216447
2000US-0216647
2000US-0216647
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2000US-0216647
2000US-0216647
2000US-0218990
2000US-022566
2000US-0225264
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 29-SEP-2000
29-SEP-2000
29-SEP-2000
20-CCT-2000
20-CCT
 WPI;
                            Rosen
2001-451937/48
                            CA,
                            Barash
                                                                                2000US-0235368
2000US-0235369
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2000US-0235679
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2000US-0237039
2000US-0241785
2000US-0241787
2000US-02411808
2000US-02411816
2000US-02418186
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2000US-0249211
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2000US-0251899
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ID 9724
AAK 0972
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to novel genes (AAL34669-AAL37666) and proteins CC (ABB03087-ABB04109) associated with the musculoskeletal system useful CC for preventing, treating or ameliorating medical conditions e.g. by CC protein or gene therapy. The genes are isolated from a range of human CC tissues disclosed in the specification. The nucleic acids, proteins, cCC antibodies and (ant)agonists are useful in the diagnosis, treatment CC and prevention of: (a) cancer, e.g. breast and ovarian cancer and CC other cancers of the adrenal gland, bone, bone marrow, breast, CC gastrointestinal tract, liver, lung, or urogenital; (b) immune CC disorders e.g. Addison's disease, allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, CC multiple sclerosis, rheumatoid arthritis and ulcerative colitis; CC colitis cardiovascular disorders such as myocardial ischaemias; (d) wound constitute in the colorious diseases e.g. cerebral anoxia and epilepsy; candiditic infectious diseases such as viral, bacterial, fungal and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local
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     31 - JAN - 2000;

04 - FEB - 2000;

24 - FEB - 2000;

02 - MAR - 2000;

16 - MAR - 2000;

17 - MAR - 2000;

18 - APR - 2000;

19 - MAY - 2000;

07 - JUN - 2000;

28 - JUN - 2000;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human immune/haematopoietic antigen genomic sequence SEQ
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parasitic infections.

Note: The sequence data for this patent did not form part of Note: The sequence data for this patent did not form part of Note: The sequence data for this patent did not form part of Note: The sequence data for this patent did not form part of Note: The sequence data for this patent did not form part of Note: The sequence data for this patent did not form part of Note: The sequence data for this patent did not form part of Note: The sequence data for this patent did not form part of Note: The sequence data for this patent did not form part of Note: The sequence data for this patent did not form part of Note: The sequence data for this patent did not form part of Note: The sequence data for this patent did not form part of Note: The sequence data for this patent did not form part of Note: The sequence data for this patent did not form part of Note: The sequence data for this patent did not form part of Note: The sequence data for this patent did not form part of Note: The sequence data for this patent did not form part of Note: The sequence data for this patent data for this patent
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atic; gene therapy; vaccine; metastasis; ds.
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21; Conservative
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     2000US-0179065.

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2000US-0184664.

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2000US-018974.

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2000US-0205515.

2000US-020467.

2000US-0214886.

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2000US-0229513

2000US-0230437

2000US-0231443

2000US-0231242

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2000US-0225213

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2000US-0225214

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2000US-0225758

2000US-02257575

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2000US-02257718

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2000US-02277009

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2000US-0236367

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2000US-0235834
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2000US-0236327.
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20-OCT 2000

01-NOV 2000

08-NOV 2000

17-NOV 2000

17-NO
AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I) amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic activity, and can be used in gene therapy and vaccine production. (I) proteins and polynucleotides may be used in the prevention, diagnosis an treatment of diseases associated with inappropriate (I) expression. For example, they may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of (I) by expressing inactive proteins or to supplement the patients own production of (I). Additionally, (I)
                                                                                                                                                                                              Disclosure;
                                                                                                                                                                                                                                  metastasis
                                                                                                                                                                                                                                                   useful for
                                                                                                                                                                                                                                                                       Nucleic
                                                                                                                                                                                                                                                                                                                                                  Rosen
                                                                                                                                                                                                                                                                                                                                                                                   (HUMA-)
                                                                                                                                                                                                                                                                                                            2001-483426/52.
                                                                                                                                                                                                                                         acids encoding for preventing,
                                                                                                                                                                                                                                                                                                                                                                                     HUMAN GENOME
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                                                                                                                                                                                                                                                                                                                                                                                     SCI INC
                                                                                                                                                                                              24536;
                                                                                                                                                                                                                                                 human immune/hematopoietic diagnosing and/or treating
                                                                                                                                                                                        3071pp +
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                                                                                                                                                                                          Listing; English.
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and

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RESULT 2
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      11-JUL-2000

14-JUL-2000

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14-AUG-2000

14-AUG-2000
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30-JUN-2000;
07-JUL-2000;
07-JUL-2000;
11-JUL-2000;
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19-MAY-2000;
07-JUN-2000;
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04-FEB-2000;
24-FEB-2000;
02-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       polynucleotides may be used to produce the secreted (I), by inserting the nucleic acids into a host cell and culturing the cell to express the protein. (I) proteins and polynucleotides may be used to prevent, diagnose and treat immune/haematopoletic-related diseases, especially cancers and cancer metastases of haematopoletic-derived cells. AAK64703 to AAK87694 represent human immune/haematopoletic antigen genomic sequences from the present invention. AAK874942 to AAK84950 and AAM82169 represent sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                          16-MAR-2000;
17-MAR-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                               cytostatic;
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21; Conserv
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                             2000US-0217496.

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2000US-0216880.
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2000US-0186350.
2000US-0189874.
2000US-0199076.
2000US-0198123.
2000US-0205515.
2000US-0205467.
2000US-0214886.
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                                                                                                                                                                                                                                                                                                                                                                                                                                               therapy;
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                                                                                                                                                                                                                                                                                                                                                                                                                                               vaccine;
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                metastasis;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           cancer;
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Вb
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17-NOV-2000;
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17-NOV-2000;
17-NOV-2000;
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                                      684
                   gtgctggggctgctgggcccc
gtgctggggctgctgggcccc
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                                                                          Similarity 100.
21; Conservative
                                                                                                                                                                   38348 BP;
                                                                                                                                                                                                      sequences used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ids encoding human immune/hematopoietic antigen preventing, diagnosing and/or treating cancers -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Barash SC,
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2000US-0250160

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2000US-02511856

2000US-0251869

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                                                                                                                                                                   9411 A; 7405 C;
                                                                                          2.0%;
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Pred. No.
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                                                                                                                                                                   8303 G;
                                                                                            DB 22;
7.5;
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                                                                                                                                                                                                      the present invention
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23-AUG-2000
23-AUG-2000
23-AUG-2000
20-SEP-2000
21-SEP-2000
21-SEP

2000US-0234998. 2000US-0235484. 2000US-0235334. 2000US-0235836. 2000US-0236327. 2000US-0236367. 2000US-0236368.

2000US-0234223. 2000US-0234274. 2000US-0234997.

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2000US-0229509 2000US-0229513 2000US-0230437 2000US-0230438 2000US-0231243 2000US-0231243 2000US-0231244 2000US-0231413 2000US-0231414 2000US-0231414

2000US-0229345

2000US - 0241808 2000US - 0241809 2000US - 0244617 2000US - 0246474 2000US - 0246476 2000US - 0246476 2000US - 0246477 2000US - 0246477 2000US - 024657 2000US - 0246523 2000US - 0246524 2000US - 0246526 2000US - 0246527 2000US - 0246528 2000US - 0246538 2000US - 0246538 2000US - 0246610 2000US - 0246610 2000US - 0246611 2000US - 0246611

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2000US-0239935 2000US-0239937 2000US-0249960 2000US-0241221 2000US-0241786 2000US-0241786 2000US-0241787

2000US-0236369. 2000US-0236370. 2000US-0236802. 2000US-0237037. 2000US-0237038. 2000US-0237039. 2000US-0237040.

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RESULT 26
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Matches 20
                                                                                                                                                                                                                                                                           The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins
'brosophila; developmental biology; cell signalling; insecticide;
                     Drosophila
                                         26-MAR-2002
                                                                                 ABL15756 standard;
                                                                                                                                                                                                                                                         The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                      Claim 1; SEQ ID NO 2965; 21pp + Sequence Listing; English
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                                                              ABL15756;
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11-JUL-2000;
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les 20; Conser
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                    melanogaster expressed
                                                                                                                                                                           1.9%; Silarity 100.0%; Conservative 0;
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Pred. No.
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                    polynucleotide
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25;
                                                                                                                                                                                              23;
                                                                                                                                                                           0;
                                                                                                                                                                                                                             0 other;
                                                                                                                                                                                              Length 4466;
                     SEQ
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                                                                                                                                                                                                                                                                                                                                                                                                     1000 or more
and cell-cell
                                                                                                                                                                           0;
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AAK84952
ID AAK8
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                                                                                                                                                                                                                                                                                                 Query Match
Best Local S
Matches 20
                                                                                                                                                                                                                                                           5437
                                                                                                                                                                                     AAK84952;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Venter
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The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL116176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-ABB72072).
31-JAN-2000;
04-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-656860/75.
P-PSDB; ABB71653.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           pharmaceutical; gene;
                                     17-JAN-2001; 2001WO-US01354
                                                                                           WO200157182-A2
                                                                                                                                               cytostatic;
                                                                                                                                                                                      Human immune/haematopoietic antigen genomic sequence
                                                                                                                                                                                                                  07-NOV-2001
                                                                                                                                                                                                                                                                      AAK84952 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 6361 BP; 1759 A; 1273 C; 1395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The sequence data for this patent did not form specification, but was obtained in electronic i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; SEQ ID NO 41750; 21pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         genes from Drosophila
interactions •
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23-MAR-2000; 2000US-191637P
11-JUL-2000; 2000US-0614150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23-MAR-2001; 2001WO-US09231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Drosophila melanogaster
                                                                09-AUG-2001
                                                                                                                                                                                                                                                                                                                                                   994 gctctctgcttacgtatgcc
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                                                                                                                                                                                                                                                                                                                                     gctctctgcttacgtatgcc 5456
                                                                                                                                                           immune;
                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
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                                                                                                                                               gene
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2000US-0179065
2000US-0180628
                                                                                                                                                                                                                  (first
                                                                                                                                                           haematopoietic; immune/haematopoietic antigen; cancer;
                                                                                                                                               therapy; vaccine;
                                                                                                                                                                                                                                                                      DNA; 38272
                                                                                                                                                                                                                 entry)
                                                                                                                                                                                                                                                                                                                                                                                                       1.9%;
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a and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        detection reagent for detecting for elucidating cell signalling
                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                                         Score 20;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Myers
                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                metastasis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ΕW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             G; 1934
                                                                                                                                                                                                                                                                                                                                                                                                         DB
25;
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                                                                                                                                                                                       SEQ ID NO: 39764.
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16-MAR-2000)

11-MAR-2000)

11-MAR-2000)

20-JUN-2000)

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21-JUL-2000)

21-AUG-2000)

11-AUG-2000)

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2000US-0218290
2000US-022964
2000US-0225214
2000US-0225266
2000US-0225266
2000US-0225277
2000US-0225477
2000US-0225775
2000US-0225775
2000US-0225779
2000US-0225779
2000US-0225788
2000US-02258277
2000US-02258277
2000US-0225827
2000US-0225827
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2000US-0229344
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2000US-0233164
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2000US-0186350
2000US-0189874
2000US-0199076
2000US-0199123
2000US-0205515
2000US-0209467
2000US-0214886
2000US-0214647
2000US-0216647
2000US-0214680
2000US-0217487
2000US-0217487
   02-OCT-2000
02-OCT-2000
13-OCT-2000
21-OCT-2000
20-OCT-2000
20-OCT
                                  Nucleic acids encoding useful for preventing, metastasis -
 Disclosure; SEQ
                                                                                                                                          Rosen
                                                                                                                                                                           ( HUMA - )
                                                                                                                                         CA,
                                                                                                                                                                           HUMAN GENOME
                                                                                                                                         Barash
                                                                                                                                                                                                          2000US-0237039.
2000US-0237040.
2000US-0239937.
2000US-02440960.
2000US-0241785.
2000US-0241808.
2000US-0241808.
2000US-0246477.
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2000US-0246476.
2000US-0246673.
2000US-02466523.
2000US-0246523.
2000US-0246526.
2000US-0246526.
2000US-0246526.
2000US-0246527.
2000US-024660.
2000US-024921.
2000US-0251856.
2000US-0251868.
2000US-0251988.
2000US-0251989.
2000US-0251989.
ID NO 39764; 3071pp + Sequence Listing; English
                                                                                                                                         SC,
                                                                                                                                                                           SCI INC
                                                   human immur
diagnosing
                                                                                                                                          Ruben
                                                                                                                                          SM:
                                                   immune/hematopoietic sing and/or treating
                                                   antigen polypeptides, cancers and
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Example 19; Page 147; 182pp; English

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                                                                                                                                                                                             01-NOV-1999;
13-APR-2000;
31-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I) amino acid sequences given in AAM82170 to AAM91921. (I) have cycostatic activity, and can be used in gene therapy and vaccine production. (I) proteins and polynucleotides may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate (I) expression. For example, they may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               that affect the activity of (I) by expressing inactive proteins or to supplement the patients own production of (I). Additionally, (I) polynucleotides may be used to produce the secreted (I), by inserting the nucleic acids into a host cell and culturing the cell to express protein. (I) proteins and polynucleotides may be used to prevent, diagnose and treat immune/haematopoletic-related diseases, especially
                                                                                                                                                                                                                                                                                                                                                                                                                         Human; differentially expressed gene; anglogenesis; diagnosis; anglogenic disorder; wound healing; cancer; cardiovascular; psoriasis; vascular tumour; proliferative tumour; proliferative vitreoretinopathy; rheumatoid arthritis; Crohn's disease; atherosclerosis; endometriosis; neovascularisation; restenosis; hypertension; aneurysm; angina; myocardial infarction; chronic heart condition; osteoporosis;
               subsequent
                                                                                                                                                                                                                                                               01-NOV-2000; 2000WO-US30051
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OX40 hybridisation probe SEQ ID NO:20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAH22274;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAH22274 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 38272 BP; 9399 A; 7384 C; 8269 G; 13220 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cancers and cancer metastases of haematopoietic-derived cells. AAK64703 to AAK87694 represent human immune/haematopoietic antigen genomic sequences from the present invention. AAK54942 to AAK54950 and AAM82169
                                treating
                                              Differentially expressed
                                                                                WPI; 2001-291056/30.
                                                                                                                                                                                                                                                                                              10-MAY-2001
                                                                                                                                                                                                                                                                                                                              WO200132926-A2
                                                                                                                                                                                                                                                                                                                                                           Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                           PCR primer; hybridisation; probe;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21-AUG-2001 (first entry)
                                                                                                              Mehraban
                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                             (GETH )
                                                                                                                                                                (CURA-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     684 gtgctggggctgctgggccc 703
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mes 20; Conservative
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                                                                                                                                                              CURAGEN CORP
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               to balloon angioplasty
                                                                                                                                                                                             ; 99US-0162699.
; 2000US-0196802.
; 2000US-0703350.
                                                                                                                Gerritsen
                                expressed genes involved in angiogenesis, useful for vascular tumors, atherosclerosis and/or restenosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1.9%;
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                                                                                                              Rastelli
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
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No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB
21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22;
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Sequence

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4 T; 0

other

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CC inappropriate angiogenesis. The polypeptides may also be used as antigens cC in the production of antibodies against them and in assays to identify comodulators of their expression and activity. The antibodies and cci nate of their expression and activity. The antibodies and cci nate of their expression and activity comodulate angiogenesis. The antibodies may also be used as diagnostic companies for detecting the presence of the polypeptides in samples. CC Disorders that may be prevented, diagnosed and/or treated by the above companies of the polypeptides in samples. CC proliferative vitreoretinopathy, rheumatoid arthritis, Crohn's disease, cc atherosclerosis, overlan hyperstimulation, psoriasis, endometricals associated with neovascularisation, restences subsequent to balloon companies of the polypeptides in samples. CC appertusion, inflammatory vasculatides, Repnaud's disease and cc phyphangitis, lymphedema, wound healing and tissue repair, ischaemia cc reperfusion injury, angina, myocardial infarctions, chronic heart cc conditions, heart failure such as congestive heart failure, age-related cc macular degeneration and osteoporosis. AAH22255 to AAH22325 and AAB98322 cropresent invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention describes differentially expressed genes involved in angiogenesis (I), and the polypeptides that encode them (I) have cardiovascular activity, and can be used in the modulation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                angiogenesis. The nucleic acids and polypeptides may be used in prevention, diagnosis and treatment of diseases associated with
                                                     present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          polypeptides may be used
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AAK87821
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                                                                                                                                                                                                                                                                              RESULT
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               31-JAN-2000;
04-FEB-2000;
24-FEB-2000;
02-MAR-2000;
16-MAR-2000;
17-MAR-2000;
18-APR-2000;
19-MAY-2000;
07-JUN-2000;
                                                                                                                                                                                 Human; digestive system antigen; ulcerative colitis; infection; Hi
                                                                                                       17-JAN-2001;
                                                                                                                       02-AUG-2001
                                                                                                                                         WO200155314-A2
                                                                                                                                                                         digestive system
                                                                                                                                                                                                            Human
                                                                                                                                                                                                                            05-NOV-2001
                                                                                                                                                                                                                                            AAK87821;
                                                                                                                                                                                                                                                             AAK87821 standard; cDNA;
                                                                                                                                                                                                                                                                                                                978 ccgatggctgcctccggct 996
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                                                                                                                                                                                                                                                                                                                                                 Local
                                                                                                                                                                                                                                                                                                     1 ccgatggctgcctccggct
                                                                                                                                                                                                           digestive
                                                                                                                                                                                                                                                                                                                                         19;
                                                                                                                                                                                                                                                                                                                                                 Similarity
2000US-0179065
2000US-0180628
2000US-0184664
2000US-0188350
2000US-0189874
2000US-0199123
2000US-0199123
2000US-0205515
2000US-0205467
2000US-02194866
2000US-0215135
                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                           (first entry)
                                                                                                       2001WO-US01324
                                                                                                                                                                                                          system antigen coding sequence SEQ ID NO: 137
                                                                                                                                                                           disorder; Meckel's
                                                                                                                                                                                                                                                                                                                                                  100.0%;
                                                                                                                                                                                                                                                              637
                                                                                                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                                                                                                 Score 19;
Pred. No.
                                                                                                                                                                                                                                                              ВP
                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                 gene therapy; cancer; irschsprung's disease;
                                                                                                                                                                                                                                                                                                                                                 DB 22; 1
1.1e+02;
                                                                                                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                                                                                                         Length 19;
                                                                                                                                                                                  appendicitis;
chronic colit
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                                                                                                                                                                                   colitis;
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20-CCT-2000
20-CCT-2000
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20-CCT-2000
08-NOV-2000
017-NOV-2000
              The present invention provides the protein and coding sequences of a number of human digestive system antigens. These can be used in the diagnosis, treatment and prevention of digestive system disorders, including cancer, Meckel's diverticulum, bacterial or parasitic infections, appendicitis, Hirschsprung's disease, chronic colitis or ulcerative colitis. The present sequence is a cDNA encoding a digest
                                                                                                                                   Claim
                                                                                                                                                                 Polynucleotides encoding digestive system antigens, useful for diagnosing, treating, preventing and/or prognozing disorders digestive system, particularly cancer and cancer metastases.
                                                                                                                                                                                                                                      WPI; 20
P-PSDB;
                                                                                                                                                                                                                                                                                       Rosen
                                                                                                                                                                                                                                                                                                                       ( HUMA - )
                                                                                                                                                                                                                                      2001-502630/55.
DB; AAM92048.
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                                                                                                                                                                                                                                                                                       CA,
antigen
                                                                                                                                   SEQ
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2000US-0241808
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2000US-0246524
2000US-0246525
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2000US-0246611
2000US-0249210
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2000US-0249211
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2000US-0249211
2000US-0249216
2000US-0251988
2000US-0251856
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                                                                                                                                   ID
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                                                                                                                                                                                                                                                                                     sc,
                                                                                                                                   137;
                                                                                                                                                                                                                                                                                                                       SCI
                                                                                                                                986pp;
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                                                                                                                                  English.
                 a digestive
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2000US-0216647 2000US-0217487 2000US-0217487 2000US-0217487 2000US-022963 2000US-022951 2000US-0225216 2000US-0225266 2000US-0225266 2000US-0225266 2000US-0225275 2000US-0225275 2000US-022575 2000US-023541 2000US-023541 2000US-023541 2000US-023540 2000US-0235397 2000US-0235397 2000US-0235397 2000US-0235393 2000US-0235935 2000US-0241786 2000US-0241786

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Sequence 637 BP: 142 A: 193 C: 147 G: 150 T: 5 other;

Sequence 637 BP: 142 A: 193 C: 147 G: 150 T: 5 other;

Ouery Match
Bast Local Similarity 100.0% . Prod No. 84: 22: Length 637:
Matches 19: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

Oy 61 tyriceticigagecigag 79

Db. 362 tyriceticigagecigag 380

Search completed: June 19, 2002. 02:21:30

Job time: 3821 sec
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Result
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Maximum DB
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Perfect score:
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Copyright (c) 1993 - 2000 Compugen Ltd.
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/cgn2_6/ptodata/2/ina/5B_COMB.seq:*
/cgn2_6/ptodata/2/ina/6A_COMB.seq:*
/cgn2_6/ptodata/2/ina/6B_COMB.seq:*
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US-08-192-480A-1
US-08-192-480A-1
US-08-097-827-6
US-08-097-827-10
US-08-944-574-10
US-08-192-480A-2
US-08-984-709A-52
US-08-984-709A-52
US-08-984-709A-49
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US-08-934-386-1
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US-08-136-119-3
US-08-611-107-32
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US-08-147-784-1
                                                 FEATURE:
                                                                        HYPOTHETICAL:
                                                                                             MOLECULE TYPE:
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Sequence 34, App Sequence 15, App		Sequence 1, Appl:	Sequence 4, Appli	Sequence 26, Appl			Sequence 3, Appl	Sequence 3, Appl		-			Sequence 9, Appl	-	-	Sequence 2, Appl	Sequence 2, Appl	Sequence 5, Appl	Sequence 5, Appl	Sequence 26, App	Sequence 270, App

LIGNMENT

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COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, v
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/147,784
FILING DATE: 03-NOV-1993
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Smith, Williaim M
REGISTRATION NUMBER: 05490A-22
REFERENCE/DOCKET NUMBER: 05490A-22
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEPRAN: (415) 326-2422
INFORMATION FOR SEO ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1057 base pairs
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MEDIUM TYPE: Floppy disk
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APPLICANT: Buck, David
APPLICANT: Engleman, Edgar G.
TITLE OF INVENTION: RECEPTOR ON THE
TITLE OF INVENTION: CD4+ T-CELLS: AC
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  NAME/KEY:
LOCATION:
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CITY: Palo Alto
STATE: California
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; OTHER INFORMATION: US-08-147-784-1

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LOCATION: 15.845

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TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1057 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                                                                                                                  Best Local Similarity Matches 1056; Conserv
                                                                                                                                                                                                                                   Query Match
Best Local :
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Godfrey, Wayne
APPLICANT: Engleman, Edgar G.
TITLE OF INVENTION: LIGAND (ACT-4-L) TO
TITLE OF INVENTION: CD4+ T-CELLS
                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE:
HYPOTHETICAL:
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CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94301
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FILING DATE: 10-FEB-1994
CLASSIFICATION: 424
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                                                                                                                        19
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                                                                  GENERAL INFORMATION:
             APPLICANT: Godfrey, Wayne
APPLICANT: Buck, David
APPLICANT: Engleman, Edgar G.
TITLE OF INVENTION: RECEPTOR ON THE SURFACE
TITLE OF INVENTION: CD4+ T-CELLS: ACT-4
NUMBER OF SEQUENCES: 2
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       CORRESPONDENCE
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Best Local S
Matches 1056
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CITY: Pa
STATE: C
COUNTRY:
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TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1057 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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PRIOR APPLICATION DATA:
APPLICATION UMBER: US 08/
FILING DATE: 03-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: Smith, Willalm M
REGISTRATION NUMBER: 30,22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Smith, Willaim M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 05-
TELECOMMUNICATION INFORMATION:
TELECHONE: (415) 326-2400
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
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COMPUTER READABLE FORM:
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LOCATION: 15..845
OTHER INFORMATION:
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nes 1056; Conserv
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Pred. No. 0;
0; Mismatches
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US-08-192-480A-1
; Sequence 1, Application US/08192480A
; Patent No. 5759546
; GENERAL INFORMATION:
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                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: DISK, 3-1/2 inch
COMPUTER: IBM PC compatible
OPERATING SYSTEM: MS DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                             1020
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                             APPLICANT: Andrew D. Weinberg and Arthur A. APPLICANT: Vandenbark
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ADDRESSEE: Klarquist Sparkman Campbell
ADDRESSEE: Leigh & Whinston
STREET: 121 S.W. Salmon Street, Suite 1600
CITY: Portland
STATE: Oregon
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TRY: United States
97204
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FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Richard J. Polley, Esq.
REGISTRATION NUMBER: 28,107
REFERENCE/DOCKET NUMBER: 4282-3;
TELECOMMUNICATION INFORMATION:
TELEPHONE: (503) 226-7391
TELEFAX: (503) 226-7391
TELEFAX: (503) 228-9446
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 848 base pairs
TYPE: Nucleic acid
STRANDEDNESS: Double
TYPE: Nucleic acid
STRANDEDNESS: DOUBLE
TYPE: Linear
                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 5
US-08-097-827-6
; Sequence 6, Application US/08097827
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: CDN
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           243
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                                                                COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/097,827
FILING DATE: 23-ULI-1993
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: Novel Cytokine Which
                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Baum, Peter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        agccgctcccagaacacggtgtgccgtccgtgcggggcttctacaaacgacgtggtc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           agctccaagccgtgcaagccctgcacgtggtgtaacctcagaagtgggagtga
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: USA
ZIP: 98101
                                                                                                                                                                                         CITY: Seattle
STATE: WA
                                                                                                                                                                                                                        ADDRESSEE: Immunex Corporation STREET: 51 University Street
                                                                                                                                                                                                                                                                                                                            Goodwin, Ray
Fanslow, William
Gayle, Richard
                                                                                                                                                                                                                                                                                              OX40
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                                                                      Version
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                                                                      #1.25
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; NAME/KEY: CDS; LOCATION: 1..618; SEQUENCE DESCRIPTION: SEQ ID NO: 6: US-08-097-827-6
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                        COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURENT APPLICATION DATA:
APPLICATION NUMBER: US/08/494,574
FILING DATE: 22-JUN-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/097,827
FILING DATE: 23-JUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia A.
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2806
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
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                    TELEPHONE: 206-587-07: INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: 206-587-
INFORMATION FOR SEQ ID NO: 6:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Goodwin, Ray
APPLICANT: Fanslow, William
APPLICANT: Gayle, William
APPLICANT: Gayle, No. 5783665el Cytokine Which is a Ligand for
TITLE OF INVENTION: 0X40
NUMBER OF SEQUENCES: 13
                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: U
ZIP: 98101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local
                                                                                                                                                                                                                                                                                                                                                                                                        STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: PEXKINS, PALTICIA A.
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2806
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ANTI-SENSE: NO
IMMEDIATE SOURCE:
CLONE: MOUSE OX40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear MOLECULE TYPE: cDNA to mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION:
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No. 5783665
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 618 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                    51 University Street
                                                                                                                                                                                                                                                                                                                                                                                     USA
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ilarity 100.0%;
Conservative (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Immunex Corporation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Peter
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1;
0.0015;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 618
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US-08-494-574-6
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SEQUENCE DESCRIPTION: SEQ ID NO: 10: US-08-097-827-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 10, Applicati
GENERAL INFORMATION:
APPLICANT: Baum
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best
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                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION: TELEPHONE: 206-587-0730 INFORMATION FOR SEQ ID NO: 10:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ANTI-SENSE: NO
IMMEDIATE SOURCE:
CLONE: MOUSE 0X40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
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                                                                                                       TOPOLOGY: linear MOLECULE TYPE: CNNA HYPOTHETICAL: NO ANTI-SENSE: NO IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/097,827
FILING DATE: 23-Jul-1993
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 1317 base pairs
                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia A.
REGISTRATION NUMBER: 34,69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: Novel Cytokine Which is a Ligand for
                                                                         FEATURE:
                                   NAME/KEY:
LOCATION:
                                                                                    CLONE: MOX40Fc Mutein
                                                                                                                                                                                                  STRANDEDNESS: single
                                                                                                                                                                                                                     TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE: WA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Immunex Corporation STREET: 51 University Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Application US/08097827
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Fanslow, William
Gayle, Richard
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CDS

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424 acaaccaggcctgcaagccctggaccaa 451
404 ACAACCAGGCCTGCAAGCCCTGGACCAA 431
                                                                                                                                                                                                              nucleic acid
                                          Conservative
                                                                                                     1..618
                                                                                                                                                                                           linear
                                                                                                                                                                                 CDNA to mRNA
                                                                                                                                                                                                    single
                                                    100.0%;
                                                    2.6%; Score 28;
100.0%; Pred. No.
                                          0
                                          Mismatches
                                                             DB 1;
                                                    0.0015
                                          0
                                                            Length 618;
                                         Indels
                                         0,
                                         Gaps
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В
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                                                                                                                                                                                          ; LOCATION:
US-08-494-574-10
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                                                                      Query Match
Best Local Similarity
Matches 28; Conserv
                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-587-0730
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 1317 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Baum, Peter
APPLICANT: Goodwin, Ray
APPLICANT: Fanslow, William
APPLICANT: Fanslow, William
APPLICANT: Gayle, Richard
TITLE OF INVENTION: NO. 5783665el Cytokine Which is a Ligand for
TITLE OF INVENTION: NO. 5783665el Cytokine Which is a Ligand for
TITLE OF INVENTION: NO. 5783665el Cytokine Which is a Ligand for
TITLE OF INVENTION: NO. 5783665el Cytokine Which is a Ligand for
TITLE OF INVENTION: NO. 5783665el Cytokine Which is a Ligand for
TITLE OF INVENTION: NO. 5783665el Cytokine Which is a Ligand for
TITLE OF INVENTION: NO. 5783665el Cytokine Which is a Ligand for
TITLE OF INVENTION: NO. 5783665el Cytokine Which is a Ligand for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 23-JUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: PERKINS, PALTICIS A.
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2806
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIA RE-lease #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/494,574
FILING DATE: 22-JUN-1995
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compati
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                        FEATURE:
                                                                                                                                                                                                                                                                         IMMEDIATE SOURCE:
CLONE: MOX40FC Mutein
                                                                                                                                                                                                                                                                                                                   ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
  404
                        424 acaaccaggcctgcaagccctggaccaa 451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       424 acaaccaggcctgcaagccctggaccaa 451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Watch 2.6%; So Local Similarity 100.0%; Fines 28; Conservative 0;
                                                                                                                                                                                                                                  NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/097,827
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ACAACCAGGCCTGCAAGCCCTGGACCAA 431
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51 University Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             USA
                                                                               2.6%; So llarity 100.0%; I Conservative 0;
                                                                                                                                                                                                                                  CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 28; DB; Pred. No. 0.0 0; Mismatches
                                                                                                     Score 28;
Pred. No.
                                                                                 Mismatches
                                                                                                     DB 1;
0.0014;
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0.0014;
                                                                                                                        Length 1317;
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GENERAL INFORMATION:
                                                                                                                                                                                           Patent No.
                                                                                                                                                                                                          Sequence 52,
                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 42
TELECOMMUNICATION INFORMATION:
TELEPHONE: (503) 226-7391
TELEFAX: (503) 228-9446
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                           GENERAL
                                                                                 APPLICANT: Williams, Mark E.
APPLICANT: Stauderman, Kenneth A.
APPLICANT: Harpold, Michael M.
TITLE OF INVENTION: HUMAN CALCIUM
TITLE OF INVENTION: METHODS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGIE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Richard J. Polley,
REGISTRATION NUMBER: 28,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatibl
OPERATING SYSTEM: MS DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
                                              CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Disk, 3-1/2 inch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: TR
TITLE OF INVENTION: ME
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                                                                  NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Andrew D. APPLICANT: Vandenbark
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ADDRESSEE:
ADDRESSEE:
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              STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: Nucleic acid
STRANDEDNESS: Single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
ADDRESSEE: Heller Enrman white ..... STREET: 4250 Executive Square, Suite 700
                                                                                                                                                                                                                                                                                                   1 ATGTGCGTGGGGGCTCGGCGGCTG 24
                                                                                                                                                                         INFORMATION:
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Similarity 100.0%; Pred. No.
                                                                                                                                                                                           7, Application US/08984709A
6320032
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         E: Richard J. Polley, Esq.
E: Klarquist Sparkman Campbell
E: Leigh & Whinston
121 S.W. Salmon Street, Suite 1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     United States of America
                                                                                                                                                                                                                                                                                                                                                                       Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IBM PC compatible
                               Heller Ehrman White & McAuliffe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Polley, Esc
3ER: 28,107
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                                                                                                     HUMAN CALCIUM CHANNEL COMPOSITIONS AND
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COMPUTER READABLE FORM:

92037

COUNTRY: US

TELECOMMUNICATION INFORMATION:

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; FRAGMENT TYPE:
; ORIGINAL SOURCE:
US-08-984-709A-52
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Best Local Similarity
Matches 19; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 49,
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APPLICANT: William
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (619) 587-5360
INFORMATION FOR SEQ ID NO: 5
SEQUENCE CHARACTERISTICS:
LENGTH: 1413 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/984
FILING DATE: 02-DEC-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Seidman, Stephanie L.
REGISTRATION NUMBER: 3473
REFIERENCE/DOCKET NUMBER: 2473
TELECOMMUNICATION INFORMATION:
TELECPHONE: (619) 450-8400
                                               SOFTWARE: FASTSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/984,709A
FILING DATE: 02-DEC-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
                                                                                                                                                                                 COMPUTER READABLE FORM: MEDIUM TYPE: Diskette
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                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
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ANTI-SENSE: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES:
                                                                                                                                                  COMPUTER: IBM CONTROL OPERATING SYSTEM:
                                                                                                                                                                                                                                 COUNTRY:
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TOPOLOGY: lir
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                 NAME: Seidman, Stephanie L. REGISTRATION NUMBER: 33,779
                                                                                                                                                                                                                                                                                                                                                                                                                                                 9, Application US/08984709A
6320032
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: California
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VENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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                                                                                                                                                                  IBM Compatible
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   NUMBER:
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100.0%; Pred. No.
tive 0; Mismatc
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                                                                                                                                                                                                                                                                                                                                                                                                   Kenneth A.
                                                                                                                                                                                                                                                                               Square,
24735-9815 (formerly 6362-9815)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24735-9815 (formerly 6362-9815)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
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13;
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US-09-114-146-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1, Application US/09114146
Patent No. 6083747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                         TELEX: 904136
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (619) 587-5360
INFORMATION FOR SEQ ID NO: 6
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                  ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                 NAME: Bent, Stephen A.
REGISTATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 46
TELECOMMUNICATION INFORMATION:
                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Bent, Stephen A.
REGISTRATION NUMBER: 29,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: CI
HYPOTHETICAL: NO
ANTI-SENSE: NO
                                                                                                                                                                                     CLASSIFICATION:
PRIOR APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
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ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: HAN, Xiao
TITLE OF INVENTION:
TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                           STREET: 3000 K Street: Washington
                                                                    TELEFAX:
                                                                                                                                                                         FILING DATE:
                                                                                                                                                                                                                                    FILING DATE:
                                                                                                                                                                                                                                               APPLICATION NUMBER:
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 TYPE:
                                                                                  TELEPHONE:
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            ENGTH:
nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                            3000 K Street, N.W., Suite 500
                                                                                                                                                                                                                                                                                                                                                                     USA
                                                                      (202)672-5300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WONG, Peter M.C.
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11;
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Best Local Similarity
"~*rhes 18; Conserva
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                                                                                    US-08-934-386-1/c
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                                                      Sequence 1, Application US/08934386 Patent No. 6306636
                                                                                                                                                                                                               Query Match
Best Local S
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             GENERAL INFORMATION:
APPLICANT: Haselkorn,
APPLICANT: Gornicki,
                                                                                                                                                                                                                                                                                                                                         TELEX: 904136
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                               REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 460
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 08
FILING DATE: 06-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Bent, Stephen A.
REGISTRATION NUMBER: 29.7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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TITLE OF INVENTION:
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CORRESPONDENCE ADDRESS:
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                                                                                                                                         685 tgctggggctgctggggcc 702
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                                                                                                                                                                                                  Local Similarity 100.0%;
les 18; Conservative (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                              nucleic acid
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                                                                                                                                                                                                                                                                                                                             410 base pairs
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3000 K Street, N.W., Suite 500
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(202)672-5399
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                            Haselkorn, Robert
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Methods for Detecting Nucleic Acid
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Pred. No.
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Best Local Similarity
Matches 18: Conserv
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TELEFAX: (713) 789-2679
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                    APPLICANT: Shah, Purvi
APPLICANT: Corley, Neil C.
TITLE OF INVENTION: NEW HUMAN GROWTH REGULATOR PROTEIN
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                             OPERATING SYSTEM: DOSSOSTWARE: FASTSEQ for Windows Version 2.0 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/893,852A FILING DATE: Filed Herewith PRIOR APPLICATION DATA: APPLICATION NUMBER:
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MEDIUM TYPE: Floppy disk
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MEDIUM TYPE: Diskett
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ATTORNEY/AGENT INFORMATION:
NAME: Kitchell, Barbara S.
REGISTRATION NUMBER: 33,928
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Bandman, Olga APPLICANT: Lal, Preeti
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                   COMPUTER:
                                                                                                                                                                                                                                                   STREET: 3174 PO
CITY: Palo Alto
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TOPOLOGY: 11
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ZIP: 77210-4433
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EDNESS: single
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3174 Porter Drive
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                                                                                                                                                                                                                     USA
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                                                                                                                                             E: Diskette
IBM Compatible
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19-SEP-1997
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Pred. No.
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Query Match
Best Local Similarity
"~+~hes 18; Conserv
                                                                                       ; TOPOLOGY: 1; MOLECULE TYPE: US-08-279-270A-2
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GENERAL IN
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                       TELEFAX: 512/474-7577
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
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MEDIUM TYPE: Floppy disk
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LIBRARY: TMLR3DT01
CLONE: 508302
                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: WASYFIELD, Denise L.
REGISTRATION NUMBER: 33,732
REFERENCE/DOCKET NUMBER: UTSH:173--1/MAY
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512,730-720
TELEPHONE: 512,7474-7577
                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 3
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APPLICANT: Schroeder, Wanda T.
TITLE OF INVENTION: Epidermal Surface Antigen and Uses
TITLE OF INVENTION: Thereof
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
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nes 18; Conservative
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                                                                                                                                                             CENGTH:
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               Conservative
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100.0%; Pred. No.
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                                          Length 2488;
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US-08-188-228-53/c
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US-08-332-643-47/c
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Patent No. 559//--
Patent No. 559//--
Patent No. 579//--
Patent No. 57
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                                                                                                                                           Sequence 47, Application US/08332643 Patent No. 5639634
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Best Local Similarity
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                                                                     GENERAL INFORMATION:
APPLICANT: Suzuki
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FILING DATE: 17 APR 1992
ATTORNEY/AGENT INFORMATION:
NAME: NO. 5597725and, Greta E
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 3134
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/188,228
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CITY: Chicago
TMATE: Illinois
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PRIOR APPLICATION UNABER: US 08/049,460
PILLING DATE: 19 APR 1993
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
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CORRESPONDENCE ADDRESS:
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TITLE OF INVENTION: CADHERIN MATERIALS AND METHODS
TITLE OF INVENTION: CADHERIN MATERIALS AND METHODS NUMBER OF SEQUENCES: 56
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                                                                                                                                                                                                                                                                                                                                                                             990 GCCATCCTGGGCCTGGGC 973
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TELEX: 25-3856
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18;
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                                                                         Suzuki, Shintaro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
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; Pred. No.
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34;
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; MOLECULE TYPE:
US-08-332-643-47
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Best Local
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                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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NAME: NO. 56396348nd, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 27866,
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 346-5750
                                                                                                                                                                                                                                                          APPLICANT: Suzuki, Shintaro
TITLE OF INVENTION: CADHERIN
NUMBER OF SEQUENCES: 62
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 1
FILING DATE:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOSTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 663 gccatcctgggcctgggc 680
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APPLICATION NUMBER: US/08/332,638 FILING DATE: 01-NOV-1994
                                                                                                                                                                       CITY: Chicago
STATE: Illinois
                                                                                                                                                                                                                          ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & ADDRESSEE: Borun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (312) 984-9740
TELEX: 25-3856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: FILING DATE:
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                                                                                                                                                          COUNTRY:
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                                                                                                                                          60606
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6300 Sears Tower, 233 S. Wacker Drive
                                                                                                                                                        USA
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                                                                                                                                                                                                                                                                              CADHERIN MATERIALS AND METHODS 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1.7%; Score 18; 100.0%; Pred. No.
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34;
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Patent No.
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Best Local
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                                                                                                                               CLASSIFICATION: 435
ATTOREY/AGENT INFORMATION:
ANAME: Muthard, David A.
REGISTRATION NUMBER: 35,297
REFERENCE/DOCKET NUMBER: 1904
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908)594-3903
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
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                                                                                               TELEFAX: (908)594-4720 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/136,119
                                                                                                                                                                                                                                                                                                                                       COUNTRY: USA
ZIP: 07065-0907
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: E
TITLE OF INVENTION: FAI
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
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LENGTH: 2550 base pairs
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
                                                                               SEQUENCE CHARACTERISTICS:
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MOLECULE TYPE:
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                            TYPE: nuclei
STRANDEDNESS:
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                                                                                                                                                                                                                                                FILING DATE:
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TOPOLOGY: 11n
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TELEX: 25-3856
                TOPOLOGY:
                                                              LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US 07/872,643 FILING DATE: 17 APR 1992
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5. 5473056
                                             nucleic acid
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                                                              2647 base pairs
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                  linear
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O. Box 2000, 126 Lincoln Avenue
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FACTOR
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Pred. No.
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34;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                      TELEFAX: 312-913-0002
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 3147 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/08/781,802
FILING DATE: 10-JAN-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/694,078
FILING DATE: 07-AUG-1996
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/019,580
FILING DATE: 12-JUN-1996
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APPLICATION NUMBER: US 60/001,995
FILING DATE: 01-AUG-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: Stable Biocatalysts for Ester Hydrolysis NUMBER OF SEQUENCES: 12
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                                                                                                         MOLECULE TYPE:
 LOCATION: 245..1231
OTHER INFORMATION: /I
OTHER INFORMATION: OI
OTHER INFORMATION: T:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                   NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US 60/009,704 FILING DATE: 11-JAN-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Chicago
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                                                                                                                                                                                                                                                                                            NAME: Chao, Mark REGISTRATION NUMBER: 37,293
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                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              E: McDonnell Boehnen Hulbert & Berghoff 300 S. Wacker Drive 32nd Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               USA
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CASADABAN, Malcolm
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FONSTEIN, Michael
VONSTEIN, Veronika
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10-JAN-1997
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100.0%; Pred. No.
tive 0; Mismatc
/note= "TspA E101 sequence longest
open reading frame; other possible start codons are TTG/leu9
TTG/leu13; TTG/leu15; GTG/val43"
                                                                                                                                                                                                                                                                              95,963-E
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34;
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; NAME/KEY:
; LOCATION:
US-08-781-802-7
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US-08-694-078-7
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                        TELEFAX: 312-913-0002 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/001,995
FILING DATE: 07-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: Chao, Mark
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: APPLICANT:
                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/019,580
FILING DATE: 12-JUN-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/009,704
FILING DATE: 10-JAN-1996
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                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 3147 base pairs
TYPE: nucleic acid
STRANDENS: single
                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: 95
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-913-0001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
                                                                               FEATURE:
                                                                                              MOLECULE TYPE:
NAME/KEY: CDS
LOCATION: 245..1231
OTHER INFORMATION: //
OTHER INFORMATION: OI
OTHER INFORMATION: T
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 07
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                   NAME: Chao, Mark REGISTRATION NUMBER:
                                                                                                              TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE:
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5. 6218163
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245..1231
                                                                                                             linear
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)0 S. Wacker Drive 7th Floor
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5, John
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100.0%;
/note= "TspA E101 sequence longest
open reading frame; other possible start codons are TTG/le
TTG/leu13; TTG/leu15; GTG/val43"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US/08/694,078
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                                                                                                                                                                                                                                                                    37,293
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Pred. No.
                                                                                                                                                                                                                                                      95,963-C
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34;
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; LOCATION:
US-08-694-078-7
                                                                                       US-08-611-107-32/c
                                                                                                           RESULT
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EARLIER FILING DATE: 1996-08-07
EARLIER FILING DATE: 1996-01-11
EARLIER FILING DATE: 1996-01-11
EARLIER FILING DATE: 1996-06-12
EARLIER APPLICATION NUMBER: 60/019,580
EARLIER APPLICATION NUMBER: 08/694,078
EARLIER APPLICATION NUMBER: 08/781,802
EARLIER FILING DATE: 1996-08-08
EARLIER APPLICATION NUMBER: 08/781,802
EARLIER FILING DATE: 1997-01-10
EARLIER APPLICATION NUMBER: 08/827,810
EARLIER APPLICATION NUMBER: 08/827,810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-058-260-7; Sequence 7, Application US/09058260B; Patent No. 6218167
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APPLICANT: Alkens, John
APPLICANT: Fonstein, Michael
APPLICANT: Vonstein, Veronika
APPLICANT: Demirjian, David
APPLICANT: Casadaban, Malcolm
                               Patent No. 5801233
GENERAL INFORMATION:
                                                                      Sequence
                                                                                                                                                                                                                                      Matches
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Best Local Similarity
Matches 18; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EARLIER FILING DATE: 1997-04-11 NUMBER OF SEQ ID NOS: 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: Stable Biocatalysts for Ester Hydrolysis FILE REFERENCE: 95-963-H
                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: Description of Artificial Sequence:cloned esterase OTHER INFORMATION: gene from bacteria E101
                                                                                                                                                                                                                                                                                                                                            NAME/KEY: CDS
LOCATION: (24)
                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Artificial Sequence
APPLICANT:
APPLICANT:
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LENGTH: 3147
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                                                                                                                                                                                                                                  Local Similarity 100.0%;
les 18; Conservative 0;
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32, nt
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                                                                  Application US/08611107
 Haselkorn, Robert
Gornicki, Piotr
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245..1231
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100.0%; Pr
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0; Mismatches
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Pred. No.
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                                                                                                                                                                                                                                                 DB 4;
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Best Local Similarity 100.
Watches 18; Conservative
                                                                                                                                                                                                                                                         Sequence 2, Application US/08162146 Patent No. 5965788 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US PCT/US93/09340
FILLING DATE: 30-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US SN 08/422,560
FILLING DATE: 14-APR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Kitchell, Barbara S.
REGISTRATION NUMBER: 33,928
REFERENCE/DOCKET NUMBER: 33,928
REFERENCE/DOCKET NUMBER: ARCD:221
TELECOMMUNICATION INFORMATION:
                                                                                                                                            APPLICANT: HOUDEBINE, Louis-Ma:
APPLICANT: DEVINOY, Eve
APPLICANT: THEPOT, Dominique
TITLE OF INVENTION: Production
TITLE OF INVENTION: the Milk o
NUMBER OF SEQUENCES: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (512) 474-7577 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING CALASSIFICATION: 800
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US SN 07/956,700
FILING DATA: 02-OCT-1992
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US PCT/US93/09340
COMPUTER READABLE FORM
                                                                                                                                                                                                                                                                                                                                                                                          2300 CTGGTGCTGGGGCTGCTG 2283
                                                                                                                          CORRESPONDENCE ADDRESS
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CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                               681 ctggtgctggggctgctg 698
                 COUNTRY: USA
ZIP: 20007-5109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                       STATE:
                                                                   CITY: Washington
                                                                                        STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: Ut
ZIP: 77210
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STATE: Texas
                                                                                      ADDRESSEE: Foley & Lardner STREET: 3000 K Street, N.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 3243 base pairs
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E OF INVENTION:
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O. Box 4433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (512) 418-3000
                                                                                                                                                               Production of a Protein of Interest in the Milk of a Transgenic Mammalian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1.7%;
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                                                                                                                                                                                                                                          Louis-Marie
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Pred. No.
                                                                                        Suite 500
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34;
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MEDIUM TYPE: COMPUTER: II

IBM

PC compatible EM: PC-DOS/MS-DOS

Floppy disk

PRIOR APPLICATION DATA:

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; LOCATION:
; LOCATION:
US-08-162-146-2
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Best Local Similarity
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REGISTRATION NUMBER: 25,258
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 672-5300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/FR92/00533
FILING DATE: 12-JUN-1992
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
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LENGTH: 4157 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: FR 91/07179 FILING DATE: 12-JUN-1991 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                      APPLICANT: DEVINOY, Eve
APPLICANT: THEPOT, Dominique
TITLE OF INVENTION: Production of a Protein of Interest in
TITLE OF INVENTION: the Milk of a Transgenic Mammalian
PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        667 tcctgggcctgggcctgg 684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     901 TCCTGGGCCTGGGCCTGG 884
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: (204) 77-5399
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: nucleic acid
STRANDEDNESS: double
                                   CLASSIFICATION:
                                                 FILING DATE:
                                                                                                                                                                                                        COUNTRY:
                                                                   APPLICATION NUMBER:
                                                                                                                                                                                                                                                                        ADDRESSEE:
                                                                                                                                                                                        20007-5109
                                                                                                                                                                                                                      Washington D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WEGNER, Harold C.
                                                                                                                                                                                                                                                      E: Foley & Lardner
3000 K Street, N.W.,
                                                                                                                                                                                                        USA
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                                                                                                                                                                                                                                                                                                                                                                                            HOUDEBINE, Louis-Marie
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..3429)
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10-FEB-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%;
08/162,146
                                                                 US/09/314,127
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                                                                                                                                                                                                                                                        Suite 500
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33;
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US-09-314-127-2
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                                                                                      COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN PC-DOS/MS-DOS
SOFTWARE: PATENTIN PC-DOS/MS-DOS
SOFTWARE: PATENTIN PC-DOS/MS-DOS
SOFTWARE: PATENTIN PC-DOS/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US SN 07/956,700
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US SN 07/956,700
FILING DATE: 02-OCT-1992
PRIOR APPLICATION NUMBER: US PCT/US93/09340
FILING DATE: 30-SEP-1993
PRIOR APPLICATION NUMBER: US N 08/422,560
ETILING DATE: 14-APR-1995
APPLICATION NUMBER: US SN 08/422,560
FILING DATE: 14-APR-1995
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Patent No. 5801
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INFORMATION FOR SEQ ID NO:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 672-5300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 12-JUN-1991
ATTORNEY/AGENT INFORMATION:
NAME: WEGNER, Harold C.
                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
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LENGTH: 4157 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                  ATTORNEY/AGENT INFORMATION:
NAME: Kitchell, Barbara S
REGISTRATION NUMBER: 33,9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
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TITLE OF INVENTION:
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TELECOMMUNICATION INFORMATION:
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ZIP: 77210
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                    REFERENCE/DOCKET NUMBER:
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18; Conservative
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301233
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100.0%; Pred. No
vative 0; Mismat
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                    ARCD: 221
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RESULT 28
US-08-905-223-270
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                                                                                                                                                                                                                                            TELEFAX: (619) 235-0176
INFORMATION FOR SEQ ID NO: 27
SEQUENCE CHARACTERISTICS:
LENGTH: 316 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: DOUBLE
TOPOLOGY: LINEAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local
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TELEFAX: (512) 474-7577
INFORMATION FOR SEQ ID NO: 30:
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/905,223
                                                                                                                                                                                                                                                                                                                                                            NAME: Israelsen, Ned A.
REGISTRATION NUMBER: 29,655
REGERENCEZDOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 235-8550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Win95
                                         NAME/KEY: other
LOCATION: 212..311
LDENTIFICATION METHOD:
OTHER INFORMATION: iden
OTHER INFORMATION: reg-
OTHER INFORMATION: vrt
                                                                                                                                                                                                              ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
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APPLICANT: Duelert, Aymeric
APPLICANT: Lacroix, Bruno
TITLE OF INVENTION: 5' ESTS FOR SECRETED PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             681 ctggtgctggggctgctg 698
            NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 11748 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
                                                                                                                                                                              TISSUE TYPE: Brain
                                                                                                                                                                                                ORGANISM: Homo Sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: San Diego
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o. 6222029
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Similarity 100.0%;
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                                                           region 1..1
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Pred. No.
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30;
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; LOCATION: 179..250
; IDENTIFICATION METHOD: Von Heijne matrix
; OTHER INFORMATION: score 4.8
; OTHER INFORMATION: seq ATMVSGSSGLAXA/RL
US-08-905-223-270
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/894,818B
FILING DATE: 20-MAY-1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP96/03253
FILING DATE: 07-NOV-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 26, Applicat Patent No. 6261822 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
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Best Local
                                                                                                                                                                                                                                                                        APPLICANT: KATO, Ikunoshin
TITLE OF INVENTION: HYPERTHERMOSTABLE PROTEASE GENES
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: Browdy and Neimark
STREET: 419 Seventh Street N.W., Ste. 300
                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: APPLICANT:
                                                                                                                                                                                           COMPUTER READABLE FORM:
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IDENTIFICATION METHOD:
OTHER INFORMATION: 1den
OTHER INFORMATION: regi
OTHER INFORMATION: id a
OTHER INFORMATION: est
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LOCATION:
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OTHER INFORMATION:
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                                                                                                                                                                                                                COUNTRY: United States of America ZIP: 20004
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IDENTIFICATION METHOD:
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o. 6261822
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R INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                             MITTA, Masanori
ASADA, Kiyozo
TSUNASAWA, Susumu
                                                                                                                                                                                                                                                                                                                                                                                                                              MORISHITA, Mio
YAMAMOTO, Katsuhiko
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TAKAKURA, Hikaru
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identity 91
region 5..63
id AA135265
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id R58602
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Length 316; Indels

0;

Gaps

0,

PRIOR APPLICATION DATA:
APPLICATION NUMBER:

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; LOCATION: US-08-583-562B-5
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US-08-583-562B-5
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REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: TAKAKURA-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-5197
TELEFAX: (202) 737-3528
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 507 base pairs
TYPE: nucleic acid
STRANDENNESS: double
TODOLOGY. 110067
                                                                                                       TELEFAX: 312-474-0448
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 545 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 5, Application US/08583562B Patent No. 5922570
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Staunton, Donald
APPLICANT: Harris, Edith
TITLE OF INVENTION: Cytoplasmic Modulators of Integrin
TITLE OF INVENTION: Binding
                                                                                                                                                                                                                                                             CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 27866/33033
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/583,562B
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: JP 323285/1995
FILING DATE: 12-DEC-1995
ATTORNEY/AGENT INFORMATION:
                                                                                     MOLECULE TYPE: CDNA
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STATE: Illinois
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                                           NAME/KEY:
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233 South Wacker Drive, 6300 Sears Tower
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                                                                      Query Match 1.6%; Score 17; DB 2; I
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 17; Conservative 0; Mismatches 0;
71 gggcctggggctgagca 87
||||||||||||||||||
279 GGGCCTGGGGCTGAGCA 295
                                                                                                      Length 545;
                                                                         Indels
                                                                        0,
                                                                      Gaps
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Search completed: June 19, 2002, 02:17:34 Job time: 3675 sec

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Title:
Perfect score:
Sequence:
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length: 2000000000
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1 MCVGARRLGRGPCA
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Copyright (c) 1993 - 2000 Compugen Ltd
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I37552
OX40 homolog
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C:Species: Homo sapiens (man)
C:Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 11-Jan-2000
C:Accession: 137552
R:Latza, U: Durkop, H.; Schnittger, S.; Ringeling, J.; Eitelbach, F.; Hummel, M.; Fo
Eur. J. Immunol. 24, 677-683, 1994
A:Title: The human OX40 homolog: cDNA structure, expression and chromosomal assignmen
A; Reference number: 137552; MUID:94170844
A; Accession: 137552
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: mRNA
A; Residues: 1-277 < CRES>
A; Cross-references: EMBL:X75962; NID:g472957; PIDN:CAA53576.1; PID:g472958
C; Superfamily: CD27 antigen; NGF receptor repeat homology
                                                              RESULT
S12783
\ensuremath{\mathsf{OX40}} antigen precursor - rat \ensuremath{\mathsf{N;Alternate}} names: nerve growth factor receptor homolog
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hypothetical prote	hypothetical prote	hypothetical prote	probable membrane	hypothetical prote	hypothetical prote	probable membrane	hypothetical prote	T-cell receptor be	histone Hlb, sperm	hypothetical prote	conserved hypothet	sugE protein - Dei	probable transcrip	hypothetical prote	hypothetical prote	hypothetical prote	gro-alpha precurso	hypothetical prote	NADH dehydrogenase	trbO protein - Ent

ALIGNMENTS

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Query Match 100.0%; Score 277; DB 2; I Best Local Similarity 100.0%; Pred. No. 2.5e-260; Matches 277; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                 GPPARPITVQPTEAWPRTSQGPSTRPVEVPGGRAVAAILGLGLVLGLLGPLAILLALYLL
                                                                                                                                                                                               NTVCRPCGPGFYNDVVSSKPCKPCTWCNLRSGSERKQLCTATQDTVCRCRAGTQPLDSYK 120
                 RRDQRLPPDAHKPPGGGSFRTPIQEEQADAHSTLAKI 277
                                                                                                                             PGVDCAPCPPGHFSPGDNQACKPWINCTLAGKHTLQPASNSSDAICEDRDPPATQPQETQ 180
                                                                  GPPARPITVQPTEAWPRTSQGPSTRPVEVPGGRAVAAILGLGLVLGLLGPLAILLALYLL
RRDQRLPPDAHKPPGGGSFRTPIQEEQADAHSTLAKI
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gene ox40 protein - mouse
N;Alternate names: Ox40 antigen
C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 11-Jan-2000
C;Accession: I48700; I48343; S34377
C;Accession: I48700; I48343; S34377
C;Accession: I51, S261-S271, 1993
A;Title: Cloning of mouse Ox40: a T cell activation marker that may mediate T-B cell A;Reference number: I48700; MUID:94044750
A;Accession: I48700
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-272 <RES>
A;Cross-references: EMBL:221674; NID:g312827; PIDN:CAA79772.1; PID:g312828
R;Birkeland, M.L.; Copeland, N.G.; Gilbert, D.J.; Jenkins, N.A.; Barclay, A.N.
Eur. J. Immunol. 25, 926-930, 1995
A:Title: Cana structure and chromosomal localization of the mouse homologue of rat O:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C:Species: Rattus norvegicus (Norway rat)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 05-Nov-1999
C:Accession: S12783; S08036
R:Mallett, S: Fossum, S: Barclay, A.N.
EMBO J. 9, 1063-1068, 1990
A:Title: Characterization of the MRC OX40 antigen of activated CD4 positive T 1;
A:Reference number: S12783; MUID:90214614
A:Accession: S12783
A:Molecule type: mRNA
A:Residues: 1-271 <MAL>
A:Cross-references: EMBL:X17037; NID:g57830; PIDN:CAA34897.1; PID:g57831
C:Superfamily: CD27 antigen; NGF receptor repeat homology
C:Keywords: growth factor receptor; transmembrane protein
F:1-19/Domain: signal sequence #status predicted <MAT>
F:211-235/Domain: transmembrane #status predicted <MAT>
F:211-235/Domain: transmembrane #status predicted <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Title: Gene Structure and Chromosomal localization of the mouse homologue of rat OX40 A;Reference number: I48334; MUID:95255413
A;Accession: I48334
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-14,'G',16-272 <RE2>
A;Cross references: EMBL:X85214; NID:g732818; PIDN:CAA59476.1; PID:g732819
C;Genetics:
hypothetical protein C2397 (photosynthetic gene cluster) - Rhodobacter capsulatus C;Species: Rhodobacter capsulatus C;Decies: Rhodobacter capsulatus C;Date: 18-Oct-1989 #sequence_revision 18-Oct-1989 #text_change 18-Jun-1993 C!Accephiqn: F28771
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F28771
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C; Superfamily:
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ily: CD27 antigen; NGF receptor repeat
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R;Burland, V.; Plunkett III, G.; Sofia, H.J.; Daniels, D.L.; Blattner, F.R. Nucleic Acids Res. 23, 2105-2119, 1995
A;Title: Analysis of the Escherichia coli genome VI: DNA sequence of the region A;Reference number: S56314; MUID:95334362
A;Accession: S56343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: EMBL:U14003; NID:g1263172; PIDN:AAA97014.1; PID:g536959
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, August 1994
C;Genetics:
A;Start codon: GTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Species: Escherichia coli
C;Date: 28-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 08-Oct-1999
C;Accession: S56343
R;Burland, V:, Plunkett III, G:, Sofia, H.J.; Daniels, D.L.; Blattner, F.R.
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A;Title: Nucleotide and deduced polypeptide A;Reference number: A90850; MUID:84259352
A;Accession: F28771
                                                                                        A; Experimental source: adult C; Genetics: A; Note: DKFZp434N1535.1
                                                                                                                                          A; Molecule type: mRNA
A; Residues: 1-151 <AAA>
A; Cross-references: EMBL: AL133575
                                                                                                                                                                                          A; Reference number: Z;
A; Accession: T43478
A; Status: preliminary
                                                                                                                                                                                                                                                                           hypothetical protein DKFZp434N1535.1 - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #tex
C;Accession: T43478
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Best Local Similarity
"---hes 8; Conserv:
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A; Residues: 1-78 < YOU>
A; Cross-references: GB: K01183
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C;Species: Escherichia coli
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7, 1984
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LGLSTVTG 28

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MHC class II alpha chain - zebra fish (C;Species: Brachydanio rerio (zebra fish) (C;Date: 13-Mar-1997 #sequence_revision 13-Mar-1997 #text_change C;Accession: 151740 R;Sultmann, H.; Mayer, W.E.; Figueroa, F.; O'Huigin, C.; Klein, Immunogenetics 38, 408-420, 1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    submitted to the EMBL Data A; Reference number: Z19565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hypothetical protein F49E12.7 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #te:
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A;Authors: Smith, H.O.; Venter, J.C.
A;Title: Genomic sequence of a Lyme disease
A;Reference number: A70100; MUID:98065943
A;Accession: E70195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R;Fraser, C.M.; Casje
son, D.; Peterson, J.
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A; Residues: 1-215 <W
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A;Experimental source: strain B31
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C.; Garland, S.;
Cn-586, 1997
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8; Conserv
                                                                                                                                                                                                                                                        Similarity
8; Conserv
                                                                                                                                                                                                                                                                                                                          3; 69/3;
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                                                                                                                                                                                                                                                       2.9%;
ilarity 100.0%;
Conservative
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MHC class II alpha chain-encoding: I51740; MUID:94011091
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                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL: Z66520; PIDN: CAA91386.1; GSPDB: GN00020;
                                                                                                                                                                                                                                                                                                                                         136/1
                                                                                                                                                                                                                                                                                                                                                                                                        clone F49E12
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     October
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                genes: polymorphism, expression,
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A;Accession: JH0749
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A;Accession: JH0749
A;Cross-references: GB:M95514; NID:g199312; PIDN:AAB46387.1; PID:g199313
A;Cross-references: GB:M95614; PID:g199312; PID:g199313
A;Cross-references: GB:M95614; PID:g199312; PID:g199312; PID:g199312; PID:g199312; PIDN:AAB46387.1; PID:g199313}
A;Cross-references: GB:M95614; PID:g199312; PID:g199312; PID:g199312; PID:g199312; PID:g199312; PI
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R;Sultmann, H.; Mayer, W.E.; Figueroa, F.; O'Huigin, Immunogenetics 38, 408-420, 1993
A;Title: Zebrafish MHC class II alpha chain-encoding A;Reference number: I51740; MUID:94011091
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A; Residues: 1-236 <SUL>
                                                                                                                                                                                                                                                                                                                                                                                                                      R;Karlsson, L.; Peterson, P.A.
J. Exp. Med. 176, 477-483, 1992
A;Title: The alpha chain gene of
A;Reference number: JH0749; MUID:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C; Accession: JH0749 R; Karlsson, L.; Pet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    class II histocompatibility antigen H-20 alpha chain precursor -
C;Species: Mus musculus (house mouse)
C;Date: 10-Jun-1993 #sequence_revision 10-Jun-1993 #text_change 2
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A;Status: preliminary; translated
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A; Residues: 1-236 <SUL>
A; Cross-references: GB:L19446; NID:g311194;
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A; Accession: I51741
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C;Date: 13-Mar-1997 #sequence_revis:
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A; Residues: 1-236 <SU2>
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8; Conservative
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Pred. No. 8.4
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conserved hypothetical protein SA1016 [imported] - Staphylococcus aureus (strain N3: C;Species: Staphylococcus aureus C;Species: Staphylococcus aureus C;Date: 10-May-2001 *sequence_revision 10-May-2001 *text_change 22-Oct-2001 C;Accession: H89888 R;Kuroda, M; Ohta, T.; Uchyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; R; Kuroda, M; Ohta, T.; Uchyama, I.; Baba, T.; Inoue, R.; Kaito, C.; Sekimizu, C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K. Lancet 357, 125-1240, 2001
A;Title: Whole genome seguencing of meticillin-resistant Stapylococcus aureus. A;Reference number: A89758; MUID:21311952; PMID:11418146
                             RESULT
S17765
                                                                                                                                                                                                                                                                                   R:Coleman, G.D.; Chen, T.H.H.
submitted to the EMBL Data Library,
A:Reference number: S31580
A:Accession: S31580
A:Status: preliminary
                                                                                                                                                                                                                                                                                                                                                            storage protein, bark - cottonwood
c;Species: Populus deltoides (cottonwood)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change
C;Accession: S31580
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S31580
 C; Species
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A;Residues: 1-329 <COL>
A;Cross-references: EMBL:X70064; NID:g20464; PID:g20465
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Best Local Similarity
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 storage protein – Carolina poplar
⊃ies⊹ Populus x canadensis (Caroli
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222 GLGLVLGL 229
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                                                                                    AALLLLGL 14
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(Carolina poplar)
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                                                                                                                                                         Score 8; 1
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BB
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B

280

AALLLIGL 287

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C;Date: 03-Feb-193.
C;Accession: S17765; S25320
R;Clausen, S.; Apel, K.
R;Clausen, S.; Apel, K.
Plant Mol. Biol. 17, 669-678, 1991
A;Title: Seasonal changes in the concentration
**Paference number: S17765; MUID:92003681
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hypothetical protein PA4219 [imported] c;Species: Pseudomonas aeruginosa C;Date: 07-Jul-1995 #sequence_revision C;Accession: C36942; G83119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT
C36942
δÃ
                                                                                                                                     A; Gene: PA4219
C; Superfamily:
                                                                                                                                                                                   A;Molecule type: DNA
A;Residues: 1-394 <STO>
A;Cross-references: GB:AE004838; GB:AE004091; NID:g9950422; PIDN:AAG07607.1; GSPDB:GN
A;Experimental source: strain PAO1
                                                                                                                                                                                                                                                                                                                                              A;Cross-references: GB:U03161; NID:g454352; PIDN:AAC43215.1; PID:g454355 R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; I adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; I Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R;Ankenbauer, R.G.; Quan, H.N.
J. Bacteriol. 176, 307-319, 1994
A;Title: FptA, the Fe(III)-pyochelin receptor of A;Reference number: A36942; MUID:94117363
A;Accession: C36942
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A;Molecule type: mRNA
A;Residues: 15-19 <CL;
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A;Note: the authors translated the codon GTG for residue
A;Note: the nucleotide sequence has been revised in refe
R;Clausen, S.; Apel, K.
Plant Mol. Biol. 20, 365, 1992
A;Tille: Seasonal changes in the concentration of the mata, Reference number: S25320; MUID:93004495
                                                                                                                                                                                                                                                                                          A;Title: Complete genome sea;Reference number: A82950;
A;Accession: G83119
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A; Accession: S17765
A; Status: preliminary
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A; Residues: 1-394 <ANK>
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A; Residues: 1-329 < CLA>
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                                       Query Match
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Matches 8
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   14 AALLLLGL 21
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                                       Similarity
8; Conserv
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                                                                                                                                     Pseudomonas aeruginosa hypothetical protein (fptA
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                                           Conservative
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                                                                                                                                                                                                                                                                                                            sequence of Pseudomonas aeruginosa PAO1,
50; MUID:20437337
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100.0%; Pred. No.
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    Pseudomonas aeruginosa

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A.; Larbig, K.; L
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probable amino acid/amine transport protein [similarity] - Escherichia coli N.Alternate names: hypothetical protein f326a C; Species: Escherichia coli C; Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 02-Nov-2001 C; Accession: B65221; S56344 R; Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; I.A.; Rose, D.J.; Mau, B.; Shao, Y. Science 277, 1453-1462, 1997 A; Title: The complete genome sequence of Escherichia coli K-12. A; Reference number: A64720; MUID:97426617 A; Accession: B65221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C; Accession: D83106
R; Stover, C.K.; Pham, X.O.; Erwin, A.L.; Mizoguch, adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; I FLORY, S.; Olson, M.V.; LORY, S.; Olson, M.V.; Nature 406, 959-964, 2000
A; Title: Complete genome sequence of Pseudomonas A; Reference number: A82950; MUID: 20437337
A; Accession: D83106
                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: GB:AE000484; GB:U00096; NID:g2367352; PIDN:AAC77076.1; PID:g2367353; A;Experimental source: strain K-12, substrain MG1655
R;Burland, V:, Plunkett III, G.; Sofia, H.J.; Daniels, D.L.; Blattner, F.R.
Nucleic Acids Res. 23, 2105-2119, 1995
A;Title: Analysis of the Escherichia coli genome VI: DNA sequence of the region from 92.
A;Reference number: S56314; MUID:95334362
A;Accession: S56314
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
RESULT
A91266
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                                                                                                                                                                                                                                                         A;Cross-references: EMBL:U14003; NID:g1263172; A;Note: the nucleotide sequence was submitted C;Superfamily: L-lysine transport protein
                                                                                                                                                                                                                                                                                                                      A; Molecule type: DNA
A; Residues: 1-321, 'SQWR', 326 <BUR>
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A; Residues: 1-445 <BLAT>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: GB:AE004848; GB:AE004091; NID:g9950537; A;Experimental source: strain PAO1
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100.0%; Pr
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L.L.; Coulter, S.N.; Folger, 
                                                                                                                                                            Score 8; DB; Pred. No. 14
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K.R.; Kas,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Escherichia coli (strain K-12
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Larbig,
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C; Accession: AF1022
C; Accession: AF1022
R; Parkhill, J.; Dougan, G.; James, R; Parkhill, J.; Cronin, A.;

K.D.; Thomson, N.R.; Pickard, D.; Davis, P.; Davies, R.M.; Dowd, L.

D.; Wain, J.; Church L.; White, N.; Farr

enterica

, S.; Moule, S.; O'Gao Nature 413, 848-852, 2 A; Authors: Parry, C.;

O'Gaora, P. 852, 2001

A; Title: Complete genome sequence

Quail, M.; Rutherford, K.; Simnome sequence of a multiple drug

Simmonds, M.; drug resistant

Skelton, J.; Steven: Salmonella enterica

se

probable amino acid permease STY4493 [imported] - Salmonella enterica subsp. C;Species: Salmonella enterica subsp. enterica serovar Typhi A;Note: this species has also been called Salmonella typhi C;Date: 09-Nov-2001 *sequence_revision 09-Nov-2001 *text_change 27-Nov-2001

AF1022

RESULT

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369

CAALLLLG

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A;Molecule type: DNA
A;Residues: 1-445 <HAY>
A;Cross-references: GB:BA000007; PIDN:BAB38520.1;
A;Experimental source: strain O157:H7, substrain F
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A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli 0157:H7 A; Reference number: A99629; MUID:21156231; PMID:11258796
A; Accession: A91266
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                                                                                                                                                                                                                                                                                                                                                                                            R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasi iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, Nature 409, 529-533, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       probable amino acid/amine transport protein [similarity] - Esche
C;Species: Escherichia coli
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change
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C;Superfamily: L-lysine
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A; Residues: 1-445 <STO>
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Best Local Similarity
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                                         2.9%; Score 8; DB ilarity 100.0%; Pred. No. 14 Conservative 0; Mismatches
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Jimalanta, E.;
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A:Reference number: AB05
A:Accession: AF1022
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-445 <PAR>
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                                                 A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-476 <STO
                                                                                                                                           A;Authors: Rutter, S.; Seeger, K.; Simon, S.; Simmonds, M.; A;Title: Massive gene decay in the leprosy bacillus. A;Reference number: A86909; MUID:21128732; PMID:11234002
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C;Superfamily: 4-coumarate--CoA ligase; acetate--CoA
F;42-469/Domain: acetate--CoA ligase homology <ACL>
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A;Cross-references: GB:Z93777; GB:AL123456; NID:g3261726; PIDN:CAB07836.1; PIDA:Experimental source: strain H37RV C;Genetics:
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A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complet A;Reference number: A70500; MUID:98295987
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C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000
C;Accession: G70607
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C;Superfamily: L-lysine transport protein
                        A;Cross-references: GB:AL450380; NID:g13093059; PIDN:CAC31432.1; GSPDB:GN00147
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Holroyd,
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A;Cross-references: GB:Z99123; GB:AL009126; NID:g2636240; PIDN:CAB15899.1; PID:e11863
A;Experimental source: strain 168
                                            A; Molecule type: DNA
A; Residues: 1-575 < KUN>
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C;Accession; D69611
C;Accession; D69611
C;Accession; D69611
C;Accession; D69611
C; Bron, S; Broulllet, S; Bruschi, C.V; Caldwell, B; Capuano, V; Carter, N.M.; A; Bron, S; Broulllet, S; Bruschi, C.V; Caldwell, B; Capuano, V; Carter, N.M.; Erilich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, A; A; Hallors; Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y; Fuma, S.; Galizzi, A.; Galizci, A; Hallors; Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y; Fuma, S.; Hosono, S; Hullo, M.; Ketter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardino A; Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Mau y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portete Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadate, V.; Sato, T.; Scanla; A; Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Se akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiya T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida A; Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A. A.; The Complete genome sequence of the Gram-positive bacterium Bacillus subtili A; Parcona, R.; Parc
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C; Genetics:
A; Gene: SP1328
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A;Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, A;Title: Complete Genome Sequence of a virulent isolate of Streptococcus A;Reference number: A95000; MUID:21357209; PMID:11463916

A;Accession: A95154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Species: Bacillus subtilis
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change
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A;Molecule type: DNA
A;Residues: 1-513 <KUR>
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C;Species: Streptococcus pneumoniae
C;Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 03-Aug-2001
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A; Status: preliminary; nucleic acid sequence
                                  A; Reference number:
A; Accession: D69611
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C;Superfamily: 4-coumarate--CoA ligase; acetate--CoA ligase homology
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8; Conser
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8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            nces: GB:AE005672; PIDN:AAK75426.1;
source: strain TIGR4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           required for expression of cytochrome bd (ATP-)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; H
White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzappl
Holt, I.E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2.9%;
100.0%;
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Pred. No.
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Pred. No.
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. 15;
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15;
   not shown;
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C;Genetics:
A;Gene: cydD
A;Gene: cydD
C;Superfamily: unassigned ATP-binding cassette proteins;
C;Keywords: ATP; nucleotide binding; P-loop
C;Keywords: ATP; binding cassette homology <ABC>
F;353-546/Domain: ATP-binding cassette homology <ABC>
F;370-377/Region: nucleotide-binding motif A (P-loop)
                                                                                                                                               A; Molecule type: mRNA
A; Residues: 1-583 <ISNA
A; Cross-references: DBJ:AB000824; NID:g2789460;
C; Superfamily; human alpha, alpha-trehalase
C; Keywords: glycosidase; hydrolase
                                                                                                                                                                                                                                                                                                 alpha,alpha-trehalase (EC 3.2.1.28) - human C;Species: Homo sapiens (man) C;Species: Homo sapiens (man) C;Date: 04-Sep-1998 #sequence_revision 04-Sep-1998 #text_change 20-Jun-2000 C;Accession: JC6504 R;Ishihara, R; Taketani, S.; Sasai-Takedatsu, M.; Kino, M.; Tokunaga, R.; Gene 202, 69-74, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: mRNA
A; Residues: 1-578 < TPS
A; Cross-references: GB: M55299; NID: g164736;
C; Superfamily: human alpha, alpha-trehalase
C; Keywords: glycosidase; hydrolase
                                                                                                                                                                                                                                gene 202, 69-74, 1997
A;Title: Molecular cloning, sequencing and A;Reference number: JC6504; MUID:98087419
A;Accession: JC6504
A;Status: preliminary
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JC6504
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A;Title: Rabbit small intestinal trebalase. Purification,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          alpha.alpha-trehalase (EC 3 2.1.28) precursor - rabbit C; Species: oryctolagus cuniculus (domestic rabbit) C; Date: 23-oct-1990 #sequence_revision 23-oct-1990 #text_change 02-Jun-2000 C; Date: A35810
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A35810
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nes 8; Conserv
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                               LLLLGLGL 23
LLLIGLGL 18
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8; Conserv
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8; Conser
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ilarity 100.0%;
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ilarity 100.0%;
Conservative
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No.
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17;
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                                                                                                  2;
                                                                                                                                                                                    PIDN:BAA24381.1; PID:g2789461
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                                                                                                                                                                                                                                                                                                                    Tokunaga, R.; Kobayashi,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cloning,
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C:Genetics:
A;Gene: ATSP:F23E12.170
A;Map position: 4
A;Introns: 307/3; 359/2; 682/1; 898/3; 962/1
C;Superfamily: Arabidopsis thaliana hypothetical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Accession: T00073
R;Nagase, T.; Ishikawa, K.; Miyajima, N.; Tanaka, A.; Kotani, DNA Res. 5, 31-39, 1998
A;Title: Prediction of the coding sequences of unidentified hua; Reference number: 214086; MUID:98290545
A;Accession: T00073
A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: mRNA
A; Residues: 1-768 < NASC;
A; Cross-references: EMBL: AB011099; NID: g3043577;
A; Experimental source: brain; clone HG2246
C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hypothetical protein KIAA0527 - human (fragment) C;Species: Homo sapiens (man) C;Date: 22-Jan-1999 #sequence_revision 22-Jan-19
R;Smith, A.G.; Pring, D.R.
Curr. Genet. 12, 617-623, 1987
Curr. Genet. 12, 617-623, 1987
A;Title: Nucleotide sequence and molecular
A;Reference number: Z14414; MUID:89003167
A;Accession: T01742
A;Status: preliminary; translated from GB/E
A;Molecule type: DNA
A;Residues: 1-52 <SMI>
                                                                                                                             hypothetical protein 3 - maize mitochondrion C:Species: mitochondrion Zea mays (maize) C:Date: 19-Feb-1999 #sequence_revision 19-Feb-1999 C:Accession: T01742
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A;Residues: 1-1031 <BEV>
A;Cross-references: EMBL:AL022604; GSPDB:GN00062; ATSP:F23E12.
A;Experimental source: cultivar Columbia; BAC clone F23E12
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T06130
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8; Conserv
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                                  translated from GB/EMBL/DDBJ
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27;
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RESULT 30

TOB512

TOB512

C:Species: Enterobacter aerogenes
C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
C:Accession: T08512
R:Thorsted, P.B.; Shah, D.S.; Macartney, D.; Kostelldou, K.; Thomas, C.M.
Plasmid 36, 95-111, 1996
A;Title: Conservation of the genetic switch between replication and transfer genes of In A; Accession: T08512
A; Reference number: Z16434; MUID:97118926
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Residues: 1-88 <THO>
A; Cross-references: EMBL:U67194; NID:g1572520; PIDN:AAC64456.1; PID:g1572561
C:Genetics: TDBC
A; Genes: trb0
Search completed: June 18, 2002, 14:29:51 Job time: 209 sec
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                                                                                                                                                                                                                                                                                                                     A; Genome: plasmid R751
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Ol-NOV-1995 (Rel. 32, Created) Ol-NOV-1995 (Rel. 32, Last sequence update) 16-CCT-2001 (Rel. 40, Last annotation update Tumor necrosis factor receptor superfamily m receptor) (ACT35 antigen) (TAX-transcription glycoprotein I receptor) (CD134 antigen). TNFRSF4 OR TXGP1L. Homo sapiens (Human). Eukaryota; Metazoa; Chordata; Craniata; Vert Mammalia; Eutheria; Primates; Catarrhini; Ho NCBI_TaxID=9606; [1] SEQUENCE FROM N.A. MEDLINE=94170844; PubMed=7510240; Latza U., Duerkop H., Schnittger S., Ringeli Hummel M., Fonatsch C., Stein H.; "The human OX40 homolog: cDNA structure, exp assignment of the ACT35 antigen."; Eur. J. Immunol. 24:677-683(1994). [2] SEQUENCE FROM N.A. MEDLINE=95219871; PubMed=7704935; Baum P.R., Gayle R.B. III, Ramsdell F., Srin Watson M.L., Seidin M.F., Clifford K.N., Gra "Identification of OX40 receptor."; CITC. Shock 44:30-34(1994)!- FUNCTION: RECEPTOR FOR THE OX40L/GP34 CY -!- SUBCELLULAR LOCATION: Type I membrane pr -!- SIMILARITY: CONTALNS 4 TNER-CYS REPEATS -!- DATABASE: NAME=PROW; NOTE=CD guide CD134 WWW="http://www.ncbi.nlm.nih.gov/prow/cd This SWISS-PROT entry is copyright. It is pr between the Swiss Institute of Bioinformati the European Bioinformatics Institute. Ther use by non-profit institute sa long a modified and this statement is not removed. entities requires a license agreement (See h or send an email to license@isb-sib.ch). EMBL; X75962; CAA53576.1; EMBL; X75962; CAA533944.1; ALT_INIT. MIM; 600315; InterPro; IPR001368; TNFR_C6.	SULT 1 IR4_HUMAN TNR4_I P4348	00 00 00 00 444440 00 00 00 00 00 00 00
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                       MEDLINE-90214614; PubMed=2157591;
Mallett S., Fossum S., Barclay A.N.;
Mallett S., Fossum S., Barclay A.N.;
Characterization of the MRC OX40 antigen of lymphocytes -- a molecule related to nerve given by 1063-1068 (1990).

EMBO J. 9:1063-1068 (1990).

-- FUNCTION: RECEPTOR FOR THE OX40L/GP34 CV:
-- SUBCELLULAR LOCATION: Type I membrane processed the support of the
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01-APR-1990 (Rel. 14, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Tumor necrosis factor receptor superfamily member receptor) (OX40 antigen) (MRC OX40).
TNFRSF4 OR TXGPIL OR OX40.
Rattus norvegicus (Rat),
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata
                                                                                                                                                                                                                                                                                                                                                                                            TNR4_RAT P15725;
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Mammalia; Eutheria;
NCBI_TaxID=10116;
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                SIMILARITY: CONTAINS 4 THER-CYS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PGVDCAPCPPGHFSPGDNQACKPWTNCTLAGKHTLQPASNSSDAICEDRDPPATQPQETQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NTVCRPCGPGFYNDVVSSKPCKPCTWCNLRSGSERKQLCTATQDTVCRCRAGTQPLDSYK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NTVCRPCGPGFYNDVVSSKPCKPCTWCNLRSGSERKQLCTATQDTVCRCRAGTQPLDSYK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    T-cell;
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29
                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; TNFR_c6; TNFR; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TNFR_NGFR_1; 3.
TNFR_NGFR_2; 2.
Antigen; Glycoprotein;
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235
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TUMOR NECROSIS FACTOR REC
SUPERFAMILY MEMBER 4.
EXTRACELLULAR (POTENTIAL)
POTENTIAL.
CYTOPLASMIC (POTENTIAL).
TNFR-CYS 1.
TNFR-CYS 2.
TNFR-CYS 3 (INCOMPLETE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0
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TNFR-CYS 4.
N-LINKED (GLCNAC. . .) (POTENTIAL)
N-LINKED (GLCNAC. . . ) (POTENTIAL);
49F15525941550BF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 277; [Pred. No. 2.6]; Mismatches
                                                                                                                                                                                                                                    Craniata; Vertebrata;
Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                            271
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                                            CYTOKINE.
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2.6e-263;
                                                                                              of active growth
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                                                                                                activated CI
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                                                                                                                                                                                                                                                                                                                          4
                                                                                                                                                                                                                                      Euteleostomi;
; Murinae; Rat
                                                                                                                                                                                                                                                                                                                        precursor
                                                                                                                  CD4
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                                                                                                  receptor
                                                                                                                positive
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RESULT 3
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Best Local S
Matches 12
                                                                                                                                                                                                                  TINRA_MOUSE SIANGLE P47741;

91-FEB-1996 (Rel. 33, Created)

10-FEB-1996 (Rel. 33, Last sequence upda'

1 16-CCT-2001 (Rel. 40, Last annotation up

""""" necrosis factor receptor superfami
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; X17037; CAA3489;
PIR; S08036; S08036.
PIR; S12783; S12783.
PISSP; P19438; 1EXT.
                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
TRANSMEM
DOMAIN
REPEAT
REPEAT
REPEAT
REPEAT
REPEAT
CARBOHYD
SEQUENCE
                      MEDLINE-95255413; PubMed-7737295; MEDLINE-95255413; PubMed-7737295; Copeland N.G., Gilbert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro: IPRO01368; TNER_c6.
pfam; pF00020; TNER_c6; 3.
proDom; pD000771; TNER_c6; 1.
SMART; SM00208; TNER; 3.
PROSTIE; PS00652; TNER_NGFR_1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Ew the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entitles requires a license agreement (See http://www.isb-sorsend an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SMART; SM00208; INC., PROSITE; PS00652; TNFR_NGFR_1; 3.
PROSITE; PS50050; TNFR_NGFR_2; 2.
PROSITE; PS50050; Antigen; Glycoprotein; Transmembrane;
                   Birkeland M.L.,
Barclay A.N.;
                                                                                Calderhead D.M., Buhlmann J.E., va
Claassen E., Noelle R.J., Fell H.;
"Cloning of mouse Ox40: a T cell a
T-B cell interactions.";
                                                                                                                                                                 Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=10090;
                                                                                                                                                                                                 receptor) (OX40 antigen).
TNFRSF4 OR TXGP1 OR OX40.
Mus musculus (Mouse).
                                                                                                                                     SEQUENCE FROM N.A. STRAIN=BALB/C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CHAIN
           "Gene
                                                                                                                         MEDLINE=94044750; PubMed=8228223;
                                                                                                                                                                                                                                                                                                                                                              138
                                                                                                                                                                                                                                                                                                                                          135
rat
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                                                                                                                                                                                                                                                                                                                                          NOACKPWINCTL
         structure
0X40
                                                                                                                                                                                                                                                                                                                                                                                 Similarity
12; Conser
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236
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61
103
124
143
271,
                                                                                                                                                                                                                                                                                                                                                                                4.3%;
ilarity 100.0%;
Conservative
protein
                                                                       151:5261-5271(1993).
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235
271
60
102
123
164
143
29895
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Rodentia;
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271
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EXTRACELLULAR (POTEN
POTENTIAL.
CYTOPLASMIC (POTENT
TNER-CYS 1.
TNER-CYS 2.
                                                                                                                                                                                                                                                                                                                                                                                  0,
                                                                                                                                                                                                                                                                                                                                                                                           Score 12;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                    TNFR-CYS 3 (INCOMPLETE).
TNFR-CYS 4.
N-LINKED (GLCNAC. .) (P.
C06465136B16EB21 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TUMOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    POTENTIAL
                                                                                                                                                                             Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                 uence update)
otation update)
superfamily member 4 precursor (0x40L)
           localization
                                                                                                                van
                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                            activation
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                                                                                                                 den
                                                                                                                                                                                                                                                                                      272
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0.00042;
0;
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                             D.J.,
                                                                                                                Eertwegh A.J.,
                                                                                                                                                                                                                                                                                      ₹
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (POTENTIAL)
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                                                                                            marker that may
           of.
                              Jenkins
                                                                                                                                                                                                                                                                                                                                                                                                      Length
           the
                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                              (POTENTIAL)
           mouse homologue
                              z
                                                                                                                                                                                                                                                                                                                                                                                                       271;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Repeat;
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TRESULT TRESULT INTERPOLATION OF CONTROL OF 
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Best Local
                                                                                                                                                                                                                                                                                                                                                                            1._MOUSE STANDARD; PR

TRIL_MOUSE STANDARD; PR

0.35305;

16-OCT-2001 (Rel. 40, Created)

16-OCT-2001 (Rel. 40, Last seque

01-MAR-2002 (Rel. 41, Last annot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; X85214; CAA59476.1; -.
HSSP; P19438; LEXT
MGD; MGI:104512; Tnfrsf4.
InterPro; IPR001368; TWFR_c6.
Pfam; PF00020; TNFR_c6; 3.
ProDom; PD000771; TNFR_c6; 1.
SMART; SM00208; TNFR; 3.
PROSITE; PS00652; TNFR_NGFR_1;
PROSITE; PS00650; TNFR_NGFR_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Signal
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                     Mus musculus (Mouse).
Eukaryota; Metazoa; C
Mammaalia; Eutheria; R
                                                                                                                                                                                                                                                                                    Tumor necrosis factor receptor superfamily member 11A precursor (Receptor activator of NF-KB) (Osteoclast differentiation factor receptor) (ODFR).

TNFRSF11A OR RANK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REPEAT
REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its
                                              Galibert L.;
                                                            TISSUE-Fetal liver;
MEDLINE-98032977; PubMed-9367155;
Anderson D.M., Maraskovsky E., Billingsley W.L., Dougall W. Tometsko M.E., Roux E.R., Teepe M.C., DuBose R.F., Cosman D
                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REPEAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; Z21674; CAA79772.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        138 NQACKPWTNCTL 149
                    homologue of the TNF receptor and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             . J. Immunol. 25:926-930(1995).
FUNCTION: RECEPTOR FOR THE OX40L/GP34 CYTOKINE.
SUBCELLULAR LOCATION: Type I membrane protein.
SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NOACKPWINCTL 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         l Similarity
12; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       T-cell;
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272
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TNFR_NGFR_2; 2.
Antigen; Glycoprotein; Transmembrane; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     211
236
272
61
103
124
165
                                                                                                                                                                                                                       Chordata;
Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30153
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ₩,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 12; DB; Pred. No. 0.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TNFR-CYS
TNFR-CYS
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TNFR-CYS 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TUMOR NECROSIS FACTOR RECEPTOR SUPERFAMILY MEMBER 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EXTRACELLULAR
                                                                                                                                                                                                                       Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -> G (IN REF. 2).
06E7BB4156F0D08E
                    its ligand
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              B 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 272;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         . .) (POTENTIAL).
                    enhance T-cell growth
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RESULT 5
                                                                                                                                                                      NAMOTINGS T., Higashio K.;

RA MOTINGS T., Higashio K.;

RY "RANK is the essential signaling receptor for osteoclast differentiation factor in osteoclastogenesis.";

RI Biochem. Biophys. Res. Commun. 253:395-400(1998).

C -!- FUNCTION: RECEPTOR FOR RANK LIGAND (RANKL; ALSO KNOWN AS OSTEOCLAST DIFFERENTIATION FACTOR OR ODF), ESSENTIAL FOR RANKL-CC MEDIATED OSTEOCLASTOGENESIS. INVOLVED IN THE REGULATION OF INTERACTIONS BETWEEN T-CELLS AND DENDRITIC CELLS.

C -!- SUBCELLULAR LOCATION: Type I membrane protein (Potential).

C -!- TISSUE SPECIFICITY: UBIQUITOUS EXPRESSION WITH HIGH LEVELS IN TRABECULAR BONE, THYMUS, SMALL INTESTINE, LUNG, BRAIN AND KIDNEY.

C -!- SIMILARITY: CONTAINS 4 THER-CYS REPEATS.
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Best Local
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REPEAT
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DOMAIN
PUFX_RHOCA STANDARD;
P26240;
01-MAY-1992 (Rel. 22, Created)
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                                                                                                                                                                                                                                                                                                                                                               CHAIN
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PROSITE; PS50050; TNFR_NGFR_2; 1.
Receptor; Glycoprotein; Transmemb
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CYTOPLASMIC (POTENTIAL).
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P42514;
01-NOV-1995
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16-OCT-2001
SEQUENCE FROM N.A. STRAIN-ATCC 15692 MEDLINE-20437337;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                              phenolate siderophore receptors.":
                                                                               Ankenbauer R.G., Quan H.N.; "FptA, the Fe(III)-pyochelin receptor of Pseudomonas aeruginosa:
                                                                                                                                                                                                                                                                                                                                                                                                                                   Photosynthesis; Membrane. SEQUENCE 78 AA; 8569 N
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15-JUL-1998 (Rel.
                                                           receptors
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                                               Bacteriol.
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SUBCELLULAR LOCATION: INTRACYTOPLASMIC MEMBRANE.
SIMILARITY: TO PUFY FROM R.SPHAEROIDES.
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F28771; F28771.
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es of the photosynthetic
polypeptides from R.
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REVISIONS.
STRAIN=KL2 / MG1655;
STRAIN=KL2 / MG1655;
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                                                                                                                                                                                                                                                                    P39269; P39268;

Ol-FEB-1995 (Rel. 31, Created)

15-JUL-1998 (Rel. 36, Last sequence up

16-OCT-2001 (Rel. 40, Last annotation

Hypothetical transport protein yjdE.

YJDE OR B4115 OR Z5717 OR ECS5097.
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Gregor J., Da
Mau B., Shao
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                                                                                                                                              STRAIN-K12 / MG1655;
MEDLINE-95334362; PubMed-7610040;
Burland V.D., Plunkett G. III, Sofia
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EMBL; AE004838; AAG07607.
                                                                                                                                                                       SEQUENCE FROM STRAIN-K12 / N
                                                                                                                                                                                                                                             Escherichia coli, and Escherichia coli 0157:H7.
                                                                                             "Analysis of the Escherichia coli genome region from 92.8 through 100 minutes."; Nucleic Acids Res. 23:2105-2119(1995).
                                                                                                                                     Blattner F.
                                                                                                                                                                                                           NCBI_TaxID=562,
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                    G. III, Bloch C.A., Perna N.T., Burl
J., Glasner J.D., Rode C.K., Mayhew
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EMBL; AE000484; AAC77076.1; -
EMBL; AE005644; AAG59314.1; -
EMBL; AP002568; BAB38520.1; -
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                                                                                                                                                                                                                        TRANSMEM TRANSMEM
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InterPro; IPR002027; Amino_acid_permease.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-0157:H7 / EDL933 / ATCC 700927;
MEDLINE-21074935; PubMed-11206551;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Science
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "The
369
                      13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUBCELLULAR LOCATION: Integral membrane protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PERMEASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIMILARITY: BELONGS TO THE ARCD/CADB/GERAB/LYSI FAMILY OF
           CAALLLLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SWISS-PROT entry is copyright. It is produced through a ceen the Swiss Institute of Bioinformatics and the EMBL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complete genome sequence of Escherichia coli K-12.";
see 277:1453-1474(1997).
CAALLLLG
                                       similarity 100.0%;
8; Conservative
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445 AA;
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                                             Score 8; DB 1; Pred. No. 5.3
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There are no restrictions on
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CYDD_BACSU
AC AC
                                       TREA_RABIT
                                                              RESULT
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Best Local
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TREA_RABIT P19813;
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-i- FUNCTION: SOMBHOW INVOLVED IN THE CYTOCHROME D BRANCH RESPIRATION. SEEMS TO BE A COMPONENT OF A TRANSPORT SY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CYDD_BACSU
P94367;
                                                                                                                                                                                                                                                                                                                    TRANSMEM
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-168 / BGSCIAI;
STRAIN-168 / BGSCIAI;
MEDLINE-97124196; PubMed-8969509;
Shindo K., Sano H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro;
InterPro;
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EMBL; Z99123; CAB15899.1; -.
HSSP; P13569; 1NBD.
Subtilist; BG11928; cydD.
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Bacteria; Firmicut
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1997 (Rel. 01-MAR-2002 (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PSO ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SMART; SM00382;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam;
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                                                                                                                                                                    232 AILLALYL 239
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUBCELLULAR LOCATION: Integral membrane protein (Probable). SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY. MSBA SUBFAMILY.
                                                                                                                            AILLALYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PF00664; ABC_membrane; PF00005; ABC_tran; 1.
                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PS00211; ABC_TRANSPORTER;
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IPR001140; ABC_transporter_tmem.
IPR003439; ABC_transportr.
IPR001687; ATP_GTP_A.
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. 35, Last sequents. 41, Last annum
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g protein cydD.
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                                                                                                                                                                                                                                                                                                                      MW:
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ATP (POTENTIAL).
FF17B481DF22A0BF CRC64;
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Pred. No.
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                      PRT;
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AL; M55299; AAA63,

PIR; A35810; A35810.

Interpro; IPR001661; Treha.

Pfam; PF01204; Trehalase; 1.

AR PRINTS; PR00744; GLHYDRLASE37.

DR PROSITE; PS00928; TREHALASE_2; 1.

PROSITE; PS00928; TREHALASE_2; 1.

OR 20, OR 22 (F.

"Vdrolase; Glycosidase; Glycoprotein; Sig.

"Val.

20 558 TREHALASE.

78 PROVED IN MATURE FOR.

FRENOVED IN MATURE FOR.

POTE.

N-LINKED (GLCNAC. . .) (POTE.

N-LINKED (GLCNAC. . .) (POTE.

9014B1189818CEAC CRC6
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                                                                     TREA_HUMAN
O43280;
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01-FEB-1991 (Rel. 17, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Trehalase precursor (EC 3.2.1.28) (Alpha,alpha-trehalase)
15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Trehalase precursor (EC 3.2.1.28) (Alpha, alpha-trehalase)
(Alpha,alpha-trehalose glucohydrolase).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -i- FUNCTION: INTESTINAL TREHALASE IS PROBABLY INVOLVED IN THE HYDROLYSIS OF INCESTED TREHALOSE.
-i- CATALYTIC ACTIVITY: Alpha.alpha-trehalose + H(2)0 = 2 D-glucose.
-i- SUBUNIT: HOMODIMER; DISULFIDE-LINKED.
-i- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor TISSUE SPECIFICITY: SMALL INTESTINE, KIDNEY, AND LESSER IN LIVING SIMILARITY: BELONGS TO FAMILY 37 OF GLYCOSYL HYDROLASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Ver
Mammalia; Eutheria; Lagomorpha; Leporidae;
MCBI_TaxID=9986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         expression, and verification anchoring.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ruf J., Wacker H., James P., Maffla M., von Kieckebusch A., Semenza G., Mantel | "Rabbit small intestinal trehalase. Pur
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A., AND F
STRAIN-NEW ZEALAND WHITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Oryctolagus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=90368681; PubMed=1697585
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Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                   Conservative
                                                                                                                                                             18
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                                                                                      STANDARD;
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Pred. No. 6.7
0; Mismatches
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                                                                                      583
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(See http://www.isb-sib.ch/announce/
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(POTENTIAL).
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ID NULM_E
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DT 15-DEC
DT 30-MAY
DE NADH-u
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   CARBOHYD
SEQUENCE
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CARBOHYD
CARBOHYD
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LIPID
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SIGNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      urine by renal proximal tubular damage.";

Nephron 73:179-185(1996).

I- FUNCTION: INTESTINAL TREHALASE IS PROBABLY INVOLVED IN THYOROLYSIS OF INGESTED TREHALOSE.

I- CAPALYTIC ACTIVITY: Alpha, alpha-trehalose + H(2)O = 2 D-1 SUBUNIT: HOMODIMER; DISULFIDE-LINKED (BY SIMILARITY).

SUBCELLULAR LOCATION: Attached to the membrane by a GPI-1 SUBCELLULAR INCENTION: ATTACHED TO THE MEMBRANES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR001661; Trehalase. Pfam; PF01204; Trehalase; 1. PR101704; Trehalase; 1. PR10175; PR00744; GLHYDRLASE37. PROSITE; PS00927; TREHALASE_1; PR0SITE; PS00928; TREHALASE_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-96369335; PubMed-8773341; MEDLINE-96369335; PubMed-8773341; Medani S., Nagata N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AB000824; BAA24381.1; -. MIM; 275360; -.
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8; Conser
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Conservative
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3EE4D31BD4D243A9 GRC64;
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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE-89139485; PubMed-2917992;
Oquendo P., Alberta J., Wen D., Graycar J.L., Derynck R.,
"The platelet-derived growth factor-inducible KC gene enco
"The platelet derived growth factor alpha-granule prote:
                                                                                                                                                                              GRO_MOUSE STANDARD; PRT; 96 AA. p12850; 01-OCT-1989 (Rel. 12, Created) 01-OCT-1989 (Rel. 12, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update) Growth regulated protein precursor (Platelet-derived inducible protein KC) (Secretory protein NS1). SCYB1 OR GRO1 OR GRO OR MGSA.
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the Euro
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MEDLINE-98292550; PubMed=9628930;
MEDLINE-98292550; PubMed=9628930;
Spruyt N., Delarbre C., Gachelin G., Laudet V.;
"Complete sequence of the amphioxus (Branchiostoma lanceolatum)
mitochondrial genome: relations to vertebrates.";
Nucleic Acids Res. 26:3279-3285(1998).
                                                                                                                             Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AF098298; AAB87993.2; ...
InterPro; IPR0013214; Mit.NADhub_oxidredctse_4L.
InterPro; IPR001133; Oxidored_q2.
Pfam; PF00420; oxidored_q2; 1.
ProDom; PD000359; Mit_NADhub_oxidredctse_4L; 1.
Oxidoreductase; NAD: Ubdquinone; Mitochondrion.
SEQUENCE 91 AA; 9751 MW; 7E7D093F02468BD3 C)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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"Complete sequence, gene arrangement, and genetic code mitochondrial DNA of the cephalochordate Branchiostoma
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MEDLINE-99261652; P
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Mol. Biol. E
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Biol. Evol. 16:410-418(1999).
CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 s SWISS-PROT entry is copyright. It is produced through ween the Swiss Institute of Bioinformatics and the EN European Bioinformatics Institute. There are no resti
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                                                                                                                                 Craniata; Vertebrata; | Sciurognathi; Muridae;
               alpha-granule proteins.";
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floridae
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EMBL; U20634; AAB03376.1; -.
EMBL; U20527; AAB03376.1; JOI
EMBL; S79767; -; NOT_ANNOTATE
PIR; A32954, 332954, 340081.
PIR; JH0081; JH0081.
HSSP; P19875; 1QNK.
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SEQUENCE
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"Two structurally distinct kappa B sequence motifs cooperative control LPS-induced KC gene transcription in mouse macrophages J. Immunol. 155:3593-3600(1995).

-i- FUNCTION: HAS CHEMOTACTIC ACTIVITY FOR NEUTROPHILS. CONTRI NEUTROPHIL ACTIVATION DURING INFLAMMATION (BY SIMILARITY).

-i- INDUCTION: BY PLATELET-DERIVED GROWTH FACTOR. IN LUNG, BY LIPOPOLYSACCHARIDE OR INFLAMMATION (BY SIMILARITY).
ELAB_ECOLI STANDARD;
P52084; Q47010;
01-OCT-1996 (Rel. 34, Created)
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Conklyn M.J., Breslow R., Showell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ryseck R.P., Macdonald-Bravo H., Matt
"Cloning and sequence of a secretory
factors in mouse fibroblasts.";
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Ryseck R.P., Macdonald-Bravo
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InterPro; IPR001089; Small_cytokine_CXC
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STRAIN=129/SV;
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SM00199; SCY; 1.
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onald-Bravo H.,
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l H.J., Gerard N.P., Gerard C.;
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STRAIN-0157:H7 / RIMD 0509952;

MEDLING-21156231; PubMed-11258796;

Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoya
Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T
Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunac
Kuhara S., Shiba T., Hattori M., Shinagawa H.;

"Complete genome sequence of enterohemorrhagic Escherichia coli
0157:H7 and genomic comparison with a laboratory strain K-12.";
DNA Res. 8:11-22(2001).
                                                                                                                                                                                                                                                                                STRAIN-0157:H7 / EDL933 / ATCC 700927;

MEDLING-21074935; PubMed-11206551;

Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,

Rose D.J., Mayhew G.F., Evan's P.S., Gregor J., Kirkpatrick H.A.,

Posfal G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,

Posfal G., Hackett J., Klink S., Boutin A., Dimalanta E.T., Potamousis K.,

Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,

Welch R.A., Blattner F.R.;
Rudd K.E.;
Unpublished observations
-|- SIMILARITY: STRONG, T
                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=K12 / MC4100;

MEDLING=96140724; PubMed=8549818;

Mueller R., Dahm C., Schulte G., Leistne

"An isochorismate hydroxymutase isogene

"EEBS Lett. 378:131-134(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Yamaamoto Y., Aiba H., Baba T., Hayashi K., Inada T., Isono K., Itoh T., Kimura S., Kitagawa M., Makino K., Miki T., Mitsuhashi N., Mizobuchi K., Mori H., Nakade S., Nakamura Y., Nashimoto H., Oshima T., Oyama S., Saito N., Sampei G., Satoh Y., Sivasundaram S. Tagami H., Takahashi H., Takeda J., Takemoto K., Uehara K., Wada C. Yamagata S., Horiuchi T.;
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Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V
Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
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Escherichia coli 0157:H7.
Bacteria, Proteobacteria;
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ace 277:1453-1474(1997).
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hara K., Wada C.,
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01-JAN-1988
15-JUL-1999
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DOMAIN
SEQUENCE
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-! SUBCELLULAR LOCATION: NUCLEAR.
-!- SIMILARITY: BELONGS TO THE HISTONE H1/H5 FAMILY.
PIR: B24560: HSDU1B.
HSSP: P02259; HST.
InterPro; IPR001316; Linker_histone.
InterPro; IPR001316; Linkerhist_N.
Pfam; PF00538; linker_histone; 1.
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Histone H1B, sperm.
Platynereis dumerilii (Dumeril's clam worm).
Platynereis dumerilii (Dumeril's clam worm).
Platynereis.
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-i- FUNCTION: HISTONES HI ARE NECESSARY FOR T
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AP002551; BAB36577.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-98298157; PubMed-9632704;
Halion S., Ford J., Foster J., Dowling L., Lucian L., Sterling M.,
Xu Y., Weiss M., Ikeda M., Liggett D., Helms A., Caux C., Lebecque S.,
Hannum C., Menon S., McClanahan T., Gorman D., Zurawski G.;
"Leukocystatin, a new class II cystatin expressed selectively by
hematopoietic cells.";
J. Biol. Chem. 273:16400-16408(1998).
J. Biol. Chem. 273:16400-16408 (1998).
J. FUNCTION: INIBITS PAPAIN AND CATHEPSIN L BUT WITH AFFINITIES
LOWER THAN OTHER CYSTATINS. MAY PLAY A ROLE IN IMMUNE REGULATION
THROUGH INHIBITION OF A UNIQUE TARGET IN THE HEMATOPOIETIC SYSTEM.
-!- SUBCELLULAR LOCATION: Secreted (Probable).
-!- SIMILARITY: BELLONGS TO THE CYSTATIN FAMILY.
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InterPro; IPR000010; Cystatin.
InterPro; IPR003243; Cystatin_C_M.
Pfam; PF00031; cystatin; 1.
ProDom; PD001231; Cystatin_C_M; 1.
                                                                                                                                                                                                                                                                                                                                                                                               the European Bioinformatics Institute. The use by non-profit institutions as not removed modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                  EMBL; AF031826; AAC40140.1;
EMBL; AF031825; AAC40139.1;
HSSP; P01038; 1A90.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. MEDLINE=98298157; Pu Halfon S., Ford J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa;
Mammalia; Eutheria;
 PR12_HORVU
                                                                                                                                                                                                                                           SIGNAL
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                                                                                                                                                                                                                                                                  PROSITE;
                                                                                                                                                                                                                                                                              SMART; SM00043; CY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=10090;
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                                                                                   231 LAILEAL 237
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                                                             LAILLAL
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llarity 100.0%;
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Rodentia;
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(Leukocystatin) (Cystatin
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POTENTIAL.
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REACTIVE SITE.
SECONDARY AREA
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                                                                                                          Score 7; DB 1;
Pred. No. 19;
0; Mismatches
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Sciurognathi;
 PRT;
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 164
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thi; Muridae;
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Murinae; Mus
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RESULT 17
PR1_HORVU
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Best Local
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                                                                                                                                PR1_HORVU STANDARD; F
Q05908;
01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last seq
01-NOV-1997 (Rel. 35, Last anno
Pathogenesis-related protein 1
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HSSP; P04284; 10...
InterPro; IPR001283; SCP.
Pfam; P70188; SCP; 1.
PRINTS; P70188; SCP; 1.
SMART; SM00198; SCP; 1.
PROSITE; PS01009; SCP_AG5_PR1_SC7_1; 1.
PROSITE; PS01009; SCP_AG5_PR1_SC7_2; 1.
PROSITE; PS010109; P
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01-JUN-1994 (Rel. 29, Last sequence
01-NOV-1997 (Rel. 35, Last annotatio
Pathogenesis-related protein PRB1-2
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Hordeum vulgare (Barley).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Trache
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Triticeae; Hordeum.
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HSSP; P04284; ICFE.
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ilarity 100.0%;
Conservative
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Last annotation update)
protein PRB1-2 precursor
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RESULT 18
CRAM_MOUSE
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CRAM_MOUSE

P51437;

P1437;

01-OCT-1996 (Rel. 34, Created)

1 01-CCT-1996 (Rel. 34, Last sequence update)

T 15-DEC-1998 (Rel. 37, Last annotation update)

Cathelin-related antimicrobial peptide precursor (Cr

14ke protein (CLP).
                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local S
Matches 7
                          SEMULENCE FROM .... STRAIN-C57BL/G; TISSUE-Bone marrow; MEDLINE-97294716; PubMed-9148921; Gallo R.L., Kim K.J., Bernfield M., Kozak C.A Merluzzi L., Gennaro R.; "Identification of CRAMP, a cathelin-related "Identification"."
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DISULFID
SEQUENCE
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SEQUENCE FROM N.A.
MEDLINE-94033324; PubMed-8219079;
MUTAGOV A., Petrasovits L., Davidson A.,
PA CDNA clone for a pathogenesis-related
Plant Mol. BLO1. 23:439-442(1993).
Plant Mol. BLO1. 23:439-442(1993).
                                                                                                                                                   Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR001283; SCP.
Pfam; PF00188; SCP; 1.
PRINTS; PR00837; V5TPXLIKE.
SMART; SM00198; SCP; 1.
              expressed
J. Biol. '
                                                                                                          SEQUENCE FROM N.A.
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PIR; S39474; S39474.
HSSP; P04284; 1CFE.
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Rodentia;
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17683
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Sciurognathi; Muridae;
                        adult mouse
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AND F
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protein 1 f
                                                                C.A.,
                                     antimicrobial peptide
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                                                                 Zanetti M.
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; Murinae; Mus
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                                                                                                                                                                                                                       (Cathelin-
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EMBL; X94353; CA
EMBL; AF035680; J
HSSP; P25230; 1L
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CONFLICT
CONFLICT
SEQUENCE
                                                                                                                                                                                                                  NU6M_ONCMY STANDARD: PRT; 173 AA. P48177; 01-FEB-1996 (Rel. 33, Created) 01-OCT-1996 (Rel. 34, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update) 16-OCT-2001 (Rel. 40, Last annotation update)
Eukaryota; Metazoa; Chordata; Craniata; Actinopterygil; Neopterygil; Teleostel; Protacanthopterygil; Salmoniformes; Salm NCBI_TaxID=8022;
                                                                                                                Oncorhynchus mykiss Mitochondrion.
                                                                                                                                                                          NADH-ubiquinone MTND6 OR ND6.
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PROSITE;
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InterPro; IPR001894; Cathelicidin.
Pfam; PF00666; Cathelicidins; 1.
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SUBMILTED (DEC-1997) to the EMBLYDBANK/DDBJ databases
-i- FUNCTION: ACTS AS A POTENT ANTIMICROBIAL PEPTIDE.
-i- TISSUE SPECIFICITY: EXPRESSED IN TESTIS, SPLEEN, STO.
INTESTINE. VERY LOW EXPRESSION FOUND IN HEART, LUNG
MUSCLE, NO EXPRESSION IN BRAIN, KINNEY OR LIVER.
-i- SIMILARITY: BELONGS TO THE CATHELICIDIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN-BALB/C; TISSUE-Bone marrow;
MEDLINE-96326596; PubMed-8706928;
MEDLINE-963265969; PubMed-8706928;
MEDLINE-9632696; PubMed-8706986
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ProDom; PD001838; Cathelicidin; 1.
PROSITE; PS00946; CATHELICIDINS_1;
PROSITE; PS00947; CATHELICIDINS_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "A novel murine cathelin-like FEBS Lett. 391:5-8(1996).
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CAA64078.1; -.
O; AAB88303.1; -.
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SIMILARITY).
BY SIMILARITY.
BY SIMILARITY.
L -> M (IN REF. 2).
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MISSING (IN REF. 1).
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Pred. No. 22;
0; Mismatches
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CATHELIN-RELATED ANTIMICROBIAL PEPTIDE.

PAUDEOL-THONE CARBOXYLIC ACID (BY
                                                                                                                                            trout) (Salmo
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                                                                                                                                                                                                         chain 6
                              Salmonidae;
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                                                         Euteleostei
                                                                                     Vertebrata;
                                                                                                                                            gairdneri)
                                                                                                                                                                                                      1.6.5.3).
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                              Oncorhynchus
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30-MAY-2000 (Rel. 39, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
NADH-ublquinone oxidoreductase chain 6 (EC 1.
MTND6 OR ND6 OR NADH6 OR NADH-6.
Salmo salar (Atlantic salmon).
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InterPro; IPR001457; Oxidored_q3.
Pfam; PP00499; oxidored_q3; 1.
Oxidoreductase; NAD; Ubiquinone; Mitochondrion.
SEQUENCE 173 AA; 18144 MW; A02134BCC15D0C3F CRC64;
                                                                                                                                                                                                                               Arnason U., Johnsson E., Rasmussen A.S.;
"The complete mitochondrial genome sequence of a teleost, Salmo and comparisons with other salmoniformes.";
Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation—the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hurst C.D., Bartlett S.E., Davidson W.S., Bruce "The complete mitochondrial DNA sequence of the salar.":
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NU6M_SALSA
Q9ZZM2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=8030
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"The complete nuclectide sequence of the mitochondrial DNA genome
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SEQUENCE FROM N.A.
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- CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol
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100.0%; Pro
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). 22;
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Matches Query Match Best Local

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EMBL; AF133701; AAF61389.1; -.
InterPro; IPR001457; Oxidored_q3.
Pfam; PF00499; oxidored_q3; 1.
Oxidoreductase; NAD; Ubiquinone; Mitochondrion.
SEQUENCE 173 AA; 18388 MW; 55322B94E972CE17 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long 
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01-APR-1993 (Rel. 25, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
01-NOV-1995 (Rel. 32, Last annotation 10 (EC 1)
NADH-ubiquinone oxidoreductase chain 10 (EC 1)
dehydrogenase 1, chain 10) (NDH-1, chain 10).
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                                                                                                                                                                                                                                                                                         EMBL; L02354; AAA25596.1; PIR; F45456; F45456.
                                                                                                                                                                                                                                                                                                                                                      entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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"DNA sequencing of the seven remaining
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                                                                                                                                                   modified and this statement is not removed entities requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a converge the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict
                                                                                                                                                                                                                                                                                                                 MEDLINE-89053719; PubMed-2461352; Young J.A., Lindsay J., Bodmer J.G., Trowsdale J.; Young J.A., Lindsay J., Bodmer J.G., Trowsdale J.; Epitope recognition by a DP alpha chain-specific (DP11.1) is influenced by the interaction between and its polymorphic DP beta chain partner."; Hum. Immunol. 23:37-44(1988).
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Strominger J.L.;
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                                                                                                                                                                                                                                                                                                                                                                                                  J. Biol.
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MEDLINE-86041930; PubMed-2997750;
Lawrance S.K., Das H.K., Pan J., Weissman
"The genomic organisation and nucleotide s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                             InterPro;
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                                                                                       3L; X03100; CAA26887.1; -.
1L; X07487; AAA633220.1; -.
3L; X00457; CAA25143.1; -.
1; A02209; HLHUSB.
1; A29313; A29313.
                                                                                                                                                                                                                                                                                                                                                                                               four genes.";
31ol. Chem. 262:8778-8786(1987).
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          PF00047; 1g; 1.
PF00993; MHC_II_alpha;
; SM00407; IGc1; 1.
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   PS00290; IG_MHC; 1.
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                                      ; Ig_MHC.
; Ig_cl.
; MHC_II_alpha.
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PRINTS; PRO0164; ABC2TRNSPORT.
PROSTTE; PS00890; ABC2_MEMBRANE; 1.
POLYSaccharide transport; Transport; Transmem 37 57 POTENTI
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P19390;
01-NOV-1990
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HAEIN
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SIGNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Capsulation in distantly related strains of Haemophilus influenzae type b: genetic drift and gene transfer at the capsulation locus.";
J. Bacteriol. 172:1374-1379(1990).
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Pfam; PF01061; ABC2_membrane; 1.
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228 LGLVLGL 234
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1990 (Rel. 16, Last sequence update)
2001 (Rel. 40, Last annotation update)
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CONNECTING PEPTIDE.
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                                                                                                                                                                                                                                                                                   use by non-profit institutions as long as its content modified and this statement is not removed. Usage by ar entitles requires a license agreement (See http://www.isb-
                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-EAGAN / SEROTYPE B;

MEDILINE-91186821; PubMed=2082145;

Kroll J.S., Loynds B., Brophy L.N., Moxon E.R.;

Kroll J.S., Loynds B., Brophy L.N., Moxon E.R.;

The bex locus in encapsulated Haemophilus influenzae: a chromosomal region involved in capsule polysaccharide export.";

Mol. Microbiol. 4:1853-1862(1990).

-i- FUNCTION: MAY FORM AN AFP-DRIVEN CAPSULE POLYSACCHARIDE EXPORT APPARATUS, IN ASSOCIATION WITH THE BEXA, BEXC AND BEXD PROTEINS.

-i- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P22235;
01-AUG-1991 (Rel. 19, Created)
01-AUG-1991 (Rel. 19, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation updat
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STRAIN=EAGAN / SEF
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Pfam; PF01061; ABC2_membrane; 1.
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; PS00890; ABC2_MEMBRANE; 1
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larity 100.0%;
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RESULT 26
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Q48215; O05081;
16-OCT-2001 (Rel. 4
16-OCT-2001 (Rel. 4
01-MAR-2002 (Rel. 4
Putative glycosyl t
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                                                                                                                                                                                                                 Hypothetical protein; Transferase; Glycosyltransferase; Complete proteome.

COMPLICT 26 26 V -> G (IN REF. 1).

CONFLICT 46 46 D -> E (IN REF. 1).

CONFLICT 49 49 F -> S (IN REF. 1).

SEQUENCE 267 AA; 30770 MW; A2F1A0532737DBC3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                        between the Swiss Institute of Bioinformatics the European Bioinformatics Institute. There a use by non-profit institutions as long as i modified and this statement is not removed. Use entities requires a license agreement (See http or send an email to license@isb-sib.ch).
LEP4_SYNY3
P72640;
                                                                                                                                                                                                                                                                                                                                   EMBL; M94855; AAA24983.1;
EMBL; U32842; AAC23341.1;
TIGR; HI1695; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=RD / KW20 / ATCC
MEDLINE=95350630; PubMed
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                                                                                                                                                                                                                                                                                                      Pfam; PF00535; Glycos_transf
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (JUN-1992) to the EMBL/GenBank/DDBJ databases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HI1695
                                                                                                                                                                                                                                                                                                                        InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Characterization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- SIMILARITY: BELONGS TO THE GLYCOSYLTRANSFERASE FAMILY 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Whole-genome random sequencing and
                                                                                      205
                                                                                                               49 GNGMVSR 55
                                                                                      GNGMVSR
                                                                                                                                            Similarity 7; Conserv
                                                                                                                                                                                                                                                                                                        IPR001173; Glycos_transf_2.
)535; Glycos_transf_2; 1.
                                                                                                                                            Conservative
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               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  40, Created)
40, Last sequence update)
41, Last annotation update)
transferase HI1695 (EC 2.-.-).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PubMed=7542800;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       u Kwaik Y., Young R., Spinola S., \lambda_1 and sequence of the lsg locus from
                                                                                                                                                        100.0%;
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                                                                                                                                                           Score 7;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           subdivision; Pasteurellaceae;
                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     assembly of Haemophilus influenzae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           267
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                                                                                                                                                        DB 1;
). 32;
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Haemophilus
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                                                                                                                                                      01-JUL-1993
01-JUL-1993
16-OCT-2001
                                     enzymes (EC 3.4.
                                                                                                                                                                                                                                                LEP4_ERWCH P31711;
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis sp. strain PCC6803. II. Sequence determination of the entire genome and assignment of potential protein-coding regions."; DNA Res. 3:109-136(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM the E
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Miyajima N., Hirosawa M., Sugiura M., Sasamoto S., Kimur
Hosouchi T., Mateuno A., Muraki A., Nakazaki N., Naruo K
Shimpo S., Takeuchi C., Wada T., Watanabe A., Yamada M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      methyltransferase (EC 2...
HOFD OR SLR1120.
Synechocystis sp. (strain
Bacteria; Cyanobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Type 4 prepilin-like proteins leader peptide processing enzyme [Includes: Leader peptidase (EC 3.4.99.-) (Prepilin peptidase);
methyltransferase (EC 2.1.1.-)}.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRINTS; PR00864; Multifunctional e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR000045; Pfam; PF01478; Peptic
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         Erwinia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. MEDLINE-97061201;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Methyltransferase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEROPS; A24.004;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; D90899; BAA16642.1;
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                                                              ymes secretion
3.4.99.-) (Pro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FUNCTION: CLEAVES TYPE-4 FIMBRIAL LEADER SEQUENCE AND THE N-TERMINAL (GENERALLY PHE) RESIDUE (BY SIMILARITY) SUBCELLURAR LOCATION: Integral membrane protein (ProbaSIMILARITY: BELONGS TO PEPTIDASE FAMILY A24; ALSO KNOW
                                                  JL-193 (Rel. 26, Created)
JL-1993 (Rel. 26, Last sequence update)
JL-1993 (Rel. 26, Last annotation update)
CT-2001 (Rel. 40, Last annotation update)
4 prepilin-like proteins leader peptide processing
5 propertion protein out0) [Includes: Leader peptide proteins out0]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GLVLGLL 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   h 2.5%;
Similarity 100.0%;
7; Conservative
      chrysanthemi
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197
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                                                                                                                                                                                                                                                                               STANDARD;
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Chroococcales;
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                                                                 N-methyltransferase (EC
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32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CRC64;
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                                                                                                                             enzyme (Pectic
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                                                                 2.1.1.-)].
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Best Local S
Matches 7
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TRANSMEM 106
TRANSMEM 128
TRANSMEM 153
TRANSMEM 176
TRANSMEM 216
TRANSMEM 259
SEQUENCE 283 AA;
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN=JAL-1 / DSM 2661 / ATCC 43057;
MEDLINE=96337999; PubMed=8688087;
MEDLINE=96337999; PubMed=8680087;
Bult C.J., White O., Olsen G.J., Zhou
Sutton G.G., Blake J.A., FitzGerald I
                                                                                                                                                               Q58052;
01-NOV-1997
                                                                                                                                                                                               METJA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the European Bioinformatics Institute. The use by non-profit institutions as not removed modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                genes from other Gram-negative bacteria.";

J. Bacteriol. 174:7385-7397(1992)
-i- FUNCTION: CLEAVES TYPE-4 FIMBRIAL LEADER SEQUENCE AND
THE N-TERMINAL (GENERALLY PHE) RESIDUE (BY SIMILARITY)
                                                                                                                     Hypothetical MJ0635.
                                                                                                                                          01-NOV-1997
16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; L02214; AA
PIR; C47755; C47
MEROPS; A24.001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lindeberg M., Collmer A.;
"Analysis of eight out genes in a secretion by Erwinia chrysanthemi:
                                                                         Methanococcus.
NCBI_TaxID=2190;
                                                                                                                                                                                                                                                                                                                                                                                                                                 PRINTS; PR00864; PREPILM Multifunctional enzyme;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM STRAIN-EC16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Proto
Pectobacterium
                                                                                                 Archaea;
                                                                                                          Methanococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         between
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- SIMILARITY: BELONGS TO
- TT LEADER PETTIDASE F
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUBCELLULAR LOCATION: Integral
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                                                                                                Euryarchaeota;
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1478; Peptidase_C20; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Proteobacteria; gamma
                                                                                                                                                                                                                                                                                2.5%;
nilarity 100.0%;
Conservative
                                                                                                                                       (Rel.
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(Rel. 35, Last sequence up
(Rel. 40, Last annotation
protein MJ0635.
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                                                                                                                                                                                   STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PubMed=1429461;
                                                                                                                                                                                                                                                                                                                                                                                                            Transmembrane; Inner
33 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5
                                                                                                                                                                                                                                                                                                                                                                                                                                  Hydrolase;
                                                                                                 Methanococcales; Methanococcaceae;
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                                                                                                                                                                                                                                                                                Score 7; DB 1; Pred. No. 34; 0; Mismatches
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           Zhou L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cluster required
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                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
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INTERPRO; IPRO00211; Gemini_BL.
Pfam; PF00845; Gemini_BL; 1.
SEQUENCE 298 AA; 33773 MW; D1E3
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Nature 301:260-262(1983).
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MEDLINE-90174930; PubMed-2308831;
MEDLINE-90174930; PubMed-2308831;
Morris B., Coates L., Lowe S., Richardson K., Eddy P.;
"Nucleotide sequence of the infectious cloned DNA components
"Nucleotide sequence of the infectious cloned DNA components
"African cassava mosaic virus (Nigerian strain).";
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Interpro; IPR000211; Gemini_BL.
Pfam; PF00845; Gemini_BL1; 1
SEQUENCE 298 AA; 33648 MW;
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Viruses; ssDNA viruses; Geminiviridae; Begomovirus
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-!- SIMILARITY: BELONGS TO GEMINIVIRUSES BL1 PROTEIN FAMILY.
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MEDILINE-99138702; PubMed-9949214;

Hughes J., Ward C.J., Aspinwall R., Butler R., Harris F
Highes J., Ward C.J., Aspinwall R., Butler R., Harris F
"Identification of a human homologue of the sea urchin
"gg jelly: a polycystic Kidney disease-like protein.";
Hum. Mol. Genet. B.543-59(1999).

EMBL, AF116459; AAD18022.1;
                          STRAIN-ZBN;
Liu Y., Kit
                                                                                             Mus spicilegus (Steppe mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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terPro; IPR00203; PKD_cys_rich.
terPro; IPR002889; REJ;
tm; PF00520; IOn_trans; 1.
tm; PF00520; PLAT; 1.
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9 (TrEMBLrel. 10, Last sequence update)
1 (TrEMBLrel. 19, Last annotation update)
KIDNEY DISEASE AND RECEPTOR FOR EGG JELLY
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Submitted (FEB-2000) to the EMBL,
EMBL; AB039073; BAB68597.1; -.
NON_TER 1 1 1
NON_TER 109 109
SEQUENCE 109 AA; 12230 MW; 81
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01-JUN-2001 (TrEMBLrel. 1
01-JUN-2001 (TrEMBLrel. 1
01-DEC-2001 (TrEMBLrel. 1
2410141K03RIK PROTEIN.
  Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
                                                                                                                                                                                                                                  Mus musculus (Mouse).
Eukaryota; Metazoa; C
Mammalia; Eutheria; F
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Submitted (DEC-1999) to the
EMBL; AL133575; CAB63722.1;
Hypothetical protein.
NON_TER 1 1
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01-MAY-2000
                                                                                                                              SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=EMBRYONIC
MEDLINE=21085660; PubMed=11217851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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01-MAY-2000
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BLrel. 13, Last sequence up
BLrel. 13, Last annotation
KDA PROTEIN (FRAGMENT).
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Rodentia;
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Sciurognathi; Muridae;
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       O51707 PRELIMINARY; PRT; 162 AA. 051707; O1-JUN-1998 (TrEMBLrel. 06, Created) O1-JUN-1998 (TrEMBLrel. 06, Last sequence up O1-JUN-2001 (TrEMBLrel. 17, Last annotation COLICIN V PRODUCTION PROTEIN, PUTATIVE.
                                                                                                                                                                                                                                                                                                                                  "Genomic sequence of a Lyme burgdorferi.";
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SEQUENCE FROM N.A.
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Nature 409:65-690(2001).
EMBL; AKO10803; BAB27191.1; -.
MGD; MGI:1915216; 2410141K03Rik.
InterPro; IPR001878; Znf_CCHC.
Pfam; PF00098; Zf-CCHC; 1.
Pfam; PF00098; Znf_CCHC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=98065943; PubMed=9403685;
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Bacteria; Spirochaetales; S
                                                                                                                                                                                                                      InterPro; IPR003825; Colic
Pfam; PF02674; Colicin_V;
                                                                                                                                                                                                                                                                        TIGR; BB0766;
                                                                                                                                                                                                                                                                             Nature 390:580-586(1997).
EMBL; AE001176; AAC67114.1;
TIGR; BB0766; -.
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221 LGLVLGLL
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                                                 Similarity
8; Conser
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162 AA;
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                                                    Conservative
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"Structure and polymorphism of the up
gene, transcriptionally regulated 'n
falciparum.";
Mol. Richer
Kawakami T., Noguchi S., Itoh T., Shige Nakajima Y., Mizuno T., Morinaga M., Ta Yamada K., Fujii Y., Ozaki K., Hirao M. Ta Yamada K., Fujii Y., Ozaki K., Hirao M. Obayashi M., Nishi T., Shibahara T., Ta Isogai T., Sugano S.; "NEDO human cDNA sequencing project.", Submitted (AUG-2000) to the EMBL/GenBar EMBL; AKO24757; BAB14988.1; -. SEQUENCE 191 AA; 20917 MW; COEBB496
                                                                                                                                                                                                                                                                                                                                                                                                   Q9H7A9
Q9H7A9;
01-MAR-2001
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01-OCT-2000 (TrEMBLrel. 15, Last sequence
01-DEC-2001 (TrEMBLrel. 19, Last annotati
HYPOTHETICAL 21, T KDA PROTEIN (FRAGMENT).
Plasmodium falciparum.
Eukaryota; Alveolata; Apicomplexa; Haemos
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01-MAR-2001 (TrEMBLrel. 16,
01-MAR-2001 (TrEMBLrel. 16,
CDNA: FLJ21104 FIS, CLONE CA
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Gentile M., Mulaa F., Alano P.;
"Repetitive sequences upstream
polymorphism in laboratory and
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MEDLINE=20520959; PubMed=11071280;
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NON_TER 1
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                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa;
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Catarrhini; Hominidae,
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M., Tanigami A., Fujiwara T., Onc
rao M., Ohmori Y., Ota T., Suzuki
T., Tanaka T., Nakamura Y.,
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Best Local Similarity
Matches 8; Conserv
SEQUENCE FROM N.A.

STRAIN-MARF303099;

MEDLIND=21082930; PubMed=11214968;

Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto Matanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura T., Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M., Takeuchi C., Yamada M., Tabata S.;
                                                                                      Sallicandro P., Paglia M.G., Hau
Gentile M., Mulaa F., Alano P.;
"Repetitive sequences upstream of
polymorphism in laboratory and of
                                                                                                                                                                            Plasmodium falciparum.
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
                                                                                                                                                                                                  01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence
01-DEC-2001 (TrEMBLrel. 19, Last annotati
HYPOTHETICAL 23.8 KDA PROTEIN (FRAGMENT).
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                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                Q9NFU4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Complete genome structure of Mesorhizobium loti."; DNA Res. 7:331-338(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rhizobium loti (Mesorhizobium loti).
Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
Phyllobacteriaceae; Mesorhizobium.
                                                                                                                                                                     NCBI_TaxID=5833;
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01-OCT-2001 (TrEMBLrel.
01-OCT-2001 (TrEMBLrel.
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                                                                  Parasitol.
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                                                                                       25 gene determine of Plasmodium
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RA Arakawa T. Hara A., Fukunishi Y. Konno H., Adachi J., Fukuda S.,
Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Kadota K., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Salito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Fruuno M., Aono H., Baldarelli R., Barsh G.,
RA Sakai K., Okido T., Fletcher C., Filta M., Gariboldi M.,
RA Blake J., Boffelli D., Hofmann M., Hume D.A., Kaniya M., Lee N.H.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kaniya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Mordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
Ra Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyo-oka K., Mang K.H., Weitz C., Whittaker C., Wilming L.,
Wanshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
                                                                                                            Matches
                                                                                                                                                             Query Match
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Best Local
                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                            PRINTS; PR00794; RIBONUCLEASE.
ProDom; PD000535; RNaseA; 1.
SMART; SM00092; RNASe_Pc; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN-C57BL/6J; TISSUE-TESTIS;
MEDLINE-21085660; PubMed-112178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-JUN-2001 (TrEMBLrel.
01-JUN-2001 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
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Q9D5A9;
                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AK015573; BAB29898.1; -.
HSSP; P00669; 1BSR.
MGD; MGI:1922269; 4930474F22Rik
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||||||||
50 VAAILGLG
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falciparum.";
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                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR001427;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hayashizaki Y.;
"Functional annotation of a full-length mouse cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nature 409:685-690(2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   930474F22RIK PROTEIN.
14
                                                 16 LLLLGLGL
                                                                                                                                      Local
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LLLLGLGL
                                                                                                         Similarity
8; Conserv
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ilarity 100.0%;
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21
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AA; 23407
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Pred. No.
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                                                                                                            Mismatches
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Best Local :
      Query Match
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Q31625;
Q31625;
Q1-ROV-1996 (TrEMBLrel. 01, C;
Q1-NOV-1996 (TrEMBLrel. 19, L;
Q1-DEC-2001 (TrEMBLrel. 19, L;
MHC CLASS II ALPHA CHAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.

MEDILINE-94011091; PubMed-8406613;

MEDILINE-94011091; PubMed-8406613;

Sultmann H., Mayer W.E., Figueroa F., O'Huigin C., Klein
"Zebrafish Mhc Class II alpha chain-encoding genes: polyn
"Zebrafish mhc tion.":
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Brachydanio rerio (Zebrafish) (Zebra danio).
Eukaryota; Metazoa; Chordata; Craniata; Vertactinopterygii; Neopterygii; Teleostei; Eute
Actinopterygii; Neopterygii; Teleostei; Eute
Cypriniformes; Cyprinidae; Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               investigating biology.";
Science 282:2012-2018(1998).
EMBL; 266520; CAA91386.1; -.
SEQUENCE 215 AA; 24861 MW;
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Thomas K.
                                                                                                                                                                                                                                                                                                         InterPro;
InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                               expression, and function.";
Immunogenetics 38:408-420(1993).
EMBL; L19450; AAA16369.1; -.
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Rhabditidae; Pelode
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                                                                                            SEQUENCE
                                                                                                                                                                                      Pfam; PF00047; ig; 1.
Pfam; PF00993; MHC_II_alpha;
SMART; SM00407; IGc1; 1.
                                                                                                                                                                                                                                                                                                                                                                      EMBL; L19446; AAA10
HSSP; P01888; 1BMG
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                                                                                                                                                         PROSITE;
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8; Conserv
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                                                                                                                                                                                                                                                                      IPR003597; Ig_cl.
IPR003006; Ig_MHC.
IPR001003; MHC_II_alpha.
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ilarity 100.0%;
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                                                                                                                                                      IG_MHC; UNKNOWN_1
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Mismatches
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DR InterPro; IPRO01003; MHC_II_alpha.
DR Pfam; PF00047; Ig; 1.
NR Pfam; PF00993; MHC_II_alpha; 1.
R SMART; SM00407; IGcl; 1.
PROSITE; PS00299; IG_MHC. "...
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                                             SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN=B10, M; TISSUE=SPLEEN;
MEDLINE=92364550; PubMed=1354242;
MEDLINE=92364550; PubMed=1354242;
Karlsson L., Peterson P.A.;
"The alpha chain gene of H-20 has al
J. Exp. Med. 176:477-483(1992).
EMBL; M95514; AAB46387.1; -.
HSSP: P01903; 1A6A.
MCD. MCD. 105024
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Q31150;
01-NOV-1996 (TrEMBLrel. C
01-NOV-1996 (TrEMBLrel. C
01-DEC-2001 (TrEMBLrel. I
01-DEC-2001 (TREMBLREL. CHAIN
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Eukaryota; Metazoa; Chordata; Craniata;
Actinopterygii; Neopterygii; Teleostei;
Cypriniformes; Cyprinidae; Danio.
                                 MGD;
                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus (Mouse)
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EMBL; L19445; AAA16367.1; -.
HSSP; P01888; 1BMG.
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MEDLINE-94011091; PubMed-8406613;

Sultmann H., Mayer W.E., Figueroa F., O'Huigin C., I
"Zebrafish MHC class II alpha chain-encoding genes:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MHC CLASS II ALPHA CHAIN.
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                              MGI:95924;
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; Ostariophysi;
                                                                                                                                                                                                                                                                                                                                                    Euteleostomi;
; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Klein J.;
polymorphism,
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RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyoswa H., Kondo S., Yamanaka I.,
RA Aizawa K., Izawa M., Nishi K., Kiyoswa H., Kondo S., Yamanaka I.,
RA Aizawa K., Izawa M., Nishi K., Kiyoswa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Kiehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashina J., Mazazarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Havyashizaki Y.;
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Matches 8
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Q9QWV1;
01-MAY-2000
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SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Sequence region.";
                                                                                                                 Nature 409:685-690(2001).
EMBL; AF100956; AAC69906.1;
EMBL; AK020594; BAB32142.1;
HSSP; P01903; 1A6A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. STRAIN-C57BL/6J; T
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InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rowen L., Qin S., Madan A., Loretz C., James R., Dors M., Mix Hall J., Lasky S., Hood L.; "Sequence of the mouse major histocomaptibility locus class II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalla; Eutherla; Rodentia;
MCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00047; 1g; 1.
Pfam; PF00993; MHC_II_alpha; 1.
SMART; SM00407; IGcl; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-C57BL/6J; TISSUE-URINARY BLADDER; MEDLINE-21085660; Pubmed-11217851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
H2-O ALPHA (HISTOCOMPATIBILITY 2, O REGION ALPHA LOCUS).
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                                                                                                                                                                                                                                   "Functional annotation of a full-length mouse cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                              [aterPro;
                                                                                                                                                                                                                                                                    łayashizaki Y.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         222
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les 8; Conservative
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IPR003597; Ig_c1.
IPR003006; Ig_MHC.
IPR001003; MHC_II_alpha.
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IPR001003; MHC_II_alpha.
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MHC CLASS II ALPHA CHAIN.
; C20A397B2EFA2004 CRC64;
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                                                                                                                                                                                                                                         collection.";
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Best Local S
Matches 8
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O9X647;
O1-NOV-1999 (TrEMBLrel. 12, Created)
O1-NOV-1999 (TrEMBLrel. 12, Last sequence update)
O1-NOV-1999 (TREMBLrel. 18, Last annotation update)
O1-OCT-2001 (TrEMBLrel. 18, Last annotation update)
HYPOTHETICAL 28.2 KDA PROTEIN.
Aeromonas hydrophila.
Racteria; Proteobacteria; gamma subdivision; Aeromo
                                                                                                                                                                Q9NPFO;
01-OCT-2000 (
01-OCT-2000 (
01-DEC-2001 (
8D6 ANTIGEN (
                                                                                                                                                                                                                                                                                                                                                                                            Aguilar A., Merino S., Nogueras M.M., Regue M., Tomas J.M.;
"Two genes from the capsule of Aeromonas hydrophila (serogroup 0:34)
confer serum resistance to Escharichia coli K-12 strains.";
Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF131869; AAD34732.1; -.
InterPro; IPR000326; PA_PFPbase.
Pfam; PF01569; PAP2; 1.
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Pfam; PF0093; MHC_II.alpha; 1.
SMART; SM00407; IGC1; 1.
PROSITE; PS00290; IG_MHC; UNKNOWN_1.
SEQUENCE 250 AA; 28166 MW; 98BCF2F8926076A1 CRC64;
 human gene
          Auffray C., Ansorge
Lehrach H., Poustka
"The European IMAGE
                                                                            Carim
                                                                                                                     Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                       Q9NPF0
                                                                                                                                                                                                                                                                                                                                                                          Hypothetical protein. SEQUENCE 264 AA; 2
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                                                                 Submitted
                                                                          SEQUENCE FROM N.A. Carim L., Estivill
                                                                                                                                                      DKFZP56401762
                                            SEQUENCE FROM
                                                                                                           NCBI_TaxID=9606;
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8; Conserv
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transcripts.";
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A., Lundebe
E consortium
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                                                                Escarceller M., Sumoy in the EMBL/GenBank/DDBJ
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15, Last sequence update)
19, Last annotation update)
2AL.29.0 KDA PROTEIN).
                     Ballabio A.,
Lundeberg J.
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Pred. No. 14;
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Pred.
                                                                                                                     Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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                                 Gibson
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Best Loc
Matches
MEDLINE-20327593; pubMed=10869091; Watanabe T., Sato H., Hatakeyama Y., M. Aizawa C., Danbara H., Maehara N.; "Cloning of the gene coding for Staphy toxin A and its expression in Escheric J. Bacteriol. 182:4101-4103(2000).
EMBL; AB036768; BAB08178.1; -. SEQUENCE 306 AA; 34379 MW; 60B7EDF
                                                                                                                                                                                                                                                                                                 Q9FDT4;
Q9FDT4;
01-MAR-2001
01-MAR-2001
01-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Li L., Zhany A.,
Choi Y.S.;
Choi Y.S.;
"Identification of a human follicular deno
stimulates germinal center B cell growth.
J. Exp. Med. 191:1077-1084(2000).
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                                                                                                                                                                                                            Staphylococcus hyicus.
Bacteria; Firmicutes; Bacillus/Staphylococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Glycoprotein
SEQUENCE 2
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                                                                                                                                                                                                                                                                EXFOLIATIVE SHETA.
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Pfam; PF00057; ldl_recept_a; 2.
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                                                                                                                                            STRAIN-P-1
                                                                                                                                                             SEQUENCE
                                                                                                                                                                                             NCBI_TaxID=1284;
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TISSUE=KIDNEY ADENOCARCINOMA;
Strausberg R.;
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r; SM00192; LDLa; 2.
r; SM00199; LDLRA_1; 7
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AL136652; CAB66587.1;
BC000668; AAH00668.1;
BC007083; AAH07083.1;
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Q43324;
01-NOV-1996
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01-DEC-2001
                                                            Populus x canadensis.

Bukaryota; Viridiplantae; Streptophyt
Spermatophyta; Magnoliophyta; eudicot
eurosids I; Malpighiales; Salicaceae;
NCBI_TaxID=3690;
                                                                                                                                                                                                                                                                                                                                                                   Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-O., Ito T., Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J., Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., S., Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.; Whole genome sequencing of meticillin-resistant Staphylococcu aureus "37:1225-1240(2001).
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           "Seasonal changes
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                     SEQUENCE FROM N.A. MEDLINE=92003681; I Clausen S., Apel K
                                                                                                                     MAJOR
                                                                                                                                                                                                                                                                                                                          Hypothetical protein; Complete SEQUENCE 315 AA; 35236 MW;
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NCBI_TaxID=158879, 158878;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation updat
PUTATIVE INTEGRAL MEMBRANE PROTEIN.
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Q93J03;
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01-MAR-2001 (TrEMBLrel.
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HYPOTHETICAL PROTEIN PAGE
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Cerdeno A.M., Parkhill J.,
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Submitted (JUN-2001)
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EMBL; S59422; AAB20113.2; -.
SEQUENCE 329 AA; 36055 MW; 875
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EMBL; AL592126; CAC42144.1; -
SEQUENCE 432 AA; 43516 MW; DC22211287
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Redenbach M., Kieser H.M., Denapaite D.,
Kinashi H., Hopwood D.A.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Actinomycetales; Streptomycineae; NCBI_TaxID=1902;
                                                                    Pseudomonas
                                                                                                  Bacteria; Proteobacteria;
                                                                                                                              Pseudomonas aeruginosa
                                                                                                                                                                   PA4323
                                                                                                                                                                                                                                                                                                                                Q9HW78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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                                  NCBI_TaxID=287;
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ilarity 100.0%;
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(TrEMBLrel. 16,
(TrEMBLrel. 18,
PROTEIN PA4323.
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                                                                                                  gamma
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                                                                                                  subdivision; Pseudomonadaceae;
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RA Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowallk D.J., Lagrou M.,
RA Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y.,
RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
RA Reizer J., Saler M.H., Hancock R.E. W., Lory S., Olson M.V.;
RT "Complete genome sequence of Pseudomonas aeruginosa PAO1, an
RT opportunistic pathogen.";
RT Nature 406:959-964 (2000).
BMBL; AE004848; AAG07711 1; -.
BMBL; AE004848; AAG07711 1; -.
BMBL; AE004848; AAG07711 1; -.
BMBL; AE004881; DUFS8; I.
SMART; SM00327; VWA; 1.
SR SMART; SM00327; VWA; 1.
SR SMART; SM00327; VWA; 1.
SO SEQUENCE 443 AA; 50359 MW; A3814456ASD5EBA8 CRC64;
                                                                                                   RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
A Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
A Alaawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
A Alitawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
A Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Hovenstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
Lyons P., Marchionni L., Mashina J., Mazazarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Sasaki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
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Q9CY76;
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5730589L02RIK PROTEIN.
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5730589L02RIK.
Mus musculus (Mouse).
Mus musculus (Motazoa; Chordata; (Motazoa; Rodentia; Motazoa; Rodentia;
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STRAIN-ATCC 15692 / PAO1:
MEDLINE-20437337; PubMed-
                "Functional annotation of a full-length Nature 409:685-690(2001).
EMBL; AK019981; BAB31950.1; -.
MGD; MGI:1924832; 5730589L02Rik
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN-C57BL/6J; TISSUE-EMBRYO;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=10090;
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Pred. No. 22;
0; Mismatches
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CE6F8E93C3D01C4F CRC64;
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XA COLE S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.
AA Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F.,
AA Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F.,
AA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
AA Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.,
AA Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
AA Oliver S., Osborne J., Quall M.A., Rajandream M.A., Rogers J.,
AA Rutter S., Seeger K., Skelton S., Squares S., Squares R.,
AS Rutter S., Seeger K., Skelton S., Squares S., Squares R.,
AB Rutter S., Seeger K., Skelton S., Squares S., Squares R.,
AB Complete genome sequence.";
AB "Deciphering the biology of Mycobacterium tuberculosis from the Complete genome sequence.";
AB LEMBL; 29377: CAB07836.1; -.
BR HSSP; P08659; 1LCI.
BR HSSP; P08659; 1LCI.
BR InterPro; IPR003015; HLH_Myc.
BR FINES, BP00151, AMP-binding; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local
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                                                                                                                                              Q50017 PRELIMINARY;
Q50017:
01-NOV-1996 (TrEMBLrel 0
01-NOV-1996 (TrEMBLrel 0
01-DEC-2001 (TrEMBLrel 1
XCLC (ACYL-COA SYNTHASE).
XCLC OR ML1051
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               005295;
005295;
01-JUL-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JUL-1997 (TrEMBLrel. 04, Last 01-DEC-2001 (TrEMBLrel. 19, Last HYPOTHETICAL 49.5 KDA PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00501; AMP-binding; 1.
PRINTS; PR00154; AMPBINDING; 1.
PROSITE; PS00455; AMP_BINDING; 1.
PROSITE; PS00038; HELIX_LOOP_HELIX; UNKNOWN_1.
Hypothetical protein; Complete proteome.
SEQUENCE 473 AA; 49520 MW; 39EEC2B0D02BAD3D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FADD36 OR RV1193 OR MTCI364.05.
SEQUENCE FROM N.A
                                                NCBI_TaxID=1769;
                                                                            Actinomycetales;
                                                                                                Bacteria; Firmicutes;
                                                                                                                          Mycobacterium leprae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=1773;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Actinomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria; Firmicutes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mycobacterium tuberculosis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 222 GLVLGLLG
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8; Conserv
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8; Conser
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llarity 100.0%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           226
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                                                                         Corynebacterineae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.
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                                                                                                Actinobacteria;
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19,
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                                                                                                                                                                                               Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 8;
Pred. No
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                                                                                                                                                                                                                                                                                                  PRT;
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annotation
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Mycobacteriaceae; Mycobacterium.
                                                                         Mycobacteriaceae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB _ 24;
                                                                                                Actinobacteridae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 473;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CRC64;
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                                                                            Mycobacterium.
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ID Q97Q97
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Best Loc
Matches
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InterPro; IPRO03015; HLH_Myc.
InterPro; IPRO03015; HLH_Myc.
Pfam; PRO0501; AMP-binding; 1.
PRINTS; PRO0154; AMPBINDING.
PROSITE; PS00455; AMP_BINDING; 1
PROSITE; PS00038; HELIX_LOOP_HEL
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097097;
01-0CT-2001
01-0CT-2001
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EMBL; U15181; AAA62961.1; -.
EMBL; AL583920; CAC31432.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-21128732; PubMed=11234002;
Cole S.T., Eiglmeier K., Parkhill J., James K.D., Thomson N.R.,
Wheeler P.R., Honore N., Garnier T., Churcher C., Harris D.,
Wheeler P.R., Basham D., Brown D., Chillingworth T., Connor R.,
Mungall K., Basham D., Brown D., Chillingworth T., Fraser A., Hamlin N.,
Davies R.M., Devlin K., Duthoy S., Feltwell T., Fraser A., Hamlin N.,
Holroyd S., Hornsby T., Jagels K., Lacroix C., Maclean J., Moule S.,
Murphy L., Oliver K., Quail M.A., Rajandream M.A., Rutter S., Seeger K., Simon S., Simmonds M., Skelton J., Squares R.,
Squares S., Stevens K., Taylor K., Whitehead S., Woodward J.R.,
                                                                                                                                                                                         Pettelin H., Nelson K.E., Paulsen I.T., Eisen J.A., Read T.D., Peterson S., Heidelberg J., DeBoy R.T., Haft D.H., Dodson R.J., Durkin A.S., Gwinn M., Kolonay J.F., Nelson W.C., Peterson J.D., Umayam L.A., White O., Salzberg S.L., Lewis M.R., Radune D., Holtzapple E., Khouri H., Wolf A.M., Utterback T.R., Hansen C.L., McDonald L.A., Feldblyum T.V., Angiuoli S., Dickinson T., Hickey Holt I.E., Loftus B.J., Yang F., Smith H.O., Venter J.C., Dougherty B.A., Morrison D.A., Hollingshead S.K., Fraser C.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Squares S.,
Barrell B.G.
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                                                                       EMBL; AE007431;
TIGR; SP1328; -
                                                                                              Science 293:498-506(2001).
EMBL; AE007431; AAK75426.1;
                                                                                                                                            "Complete genome sequence of pneumoniae.";
                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=21357209; PubMed=11463916;
                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=1313;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria; Firmicutes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Leproma; ML1051;
                                                InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          222 GLVLGLLG
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PF00474; SSF; PS00456; N
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8; Conser
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                                                IPR001734; Na_solut_symport.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (TrEMBLrel. 18, Created)
(TrEMBLrel. 18, Last sequence update)
(TrEMBLrel. 19, Last annotation updat
TE SYMPORTER FAMILY PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
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  NA_SOLUT_SYMP_1; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         50130
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                                                                                                                                                                                                                                                                                                                                                      RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Alzawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Kuchl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Kuchl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Kuchl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubhi F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Schriml L.M., Staubhi F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Frunno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carnincl P., de Bonaldo M.F.,
RA Blake J., Boffelli D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Brownstein M.J., Bult C., Fletcher C., Fijita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Myushaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashtzaki Y.,
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Best Local S
Matches 8
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Best Local
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SEQUENCE
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Complete
SEQUENCE
                                                                                                                                                                                                                                                              Hayashizaki Y.;
"Functional annotation of a full-length mouse Nature 409:685-690(2001).
EMBL; AF136944; AAF61430.1; -.
EMBL; AK008912; BAB25963.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ohta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
TREHALASE (EC 3.2.1.28) (2210412M19RIK PROTEIN).
TREH OR 2210412M19RIK.
                                                                                                                                                    PRINTS: PR00744; GLHYDRLASE37.
PROSITE; PS00927; TREHALASE_1;
PROSITE; PS00928; TREHALASE_2;
                                                                                                                                                                                                               MGD; MGI:1926230; Treh.
InterPro; IPR001661; Trehalase.
Pfam; PF01204; Trehalase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-21085660;
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Kurimoto M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-DDY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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576 AA; 65401 MW;
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do N., Ariyasu H., Yanai Y.,
                         Conservative
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; PubMed-11217851;
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Pred. No
                                           Score 8;
Pred. No.
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                                                                                                                     53CDA6A10511520E CRC64;
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5. 25;
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MEDLINE-20277482; PubMed-10819331;
MEDLINE-20277482; PubMed-10819331;
Magase T., Kikuno R., Ishikawa K., Hirosawa Prediction of the coding sequences of unide genes.XVII The complete sequences of 100 new which code for large proteins in vitro.";
DNA Res. 7:143-150(2000).

EMBL; AB040897; BAA95988.1; -.
InterPro; IPR003877; SPRY.
InterPro; IPR003878; SPRY_domain.
Pfam; PF00622; SPRY; 1.
SMART; SM00449; SPRY; 1.
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01-OCT-2000
01-OCT-2000
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SEQUENCE
InterPro; IPR000538; Link.
InterPro; IPR000436; Sushi_SCR_CCP.
Pfam; PF00084; Sushi; 1.
SMART; SM00032; CCP; 1.
SMART; SM000445; LINK; 1.
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                                                                                                               "Prediction of the coding sequences of The complete sequences of 100 new cDNA code for large proteins in vitro."; DNA Res. 5:31-39(1998)
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Mammalia; Eutheria;
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Homo sapiens (Human).
""'Parvota; Metazoa; Chordata;
"""heria; Primates;
                                                                                                                                                                                              Ohara O.
                                                                                                                                                                                                                                                    TISSUE-BRAIN;
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tes 8; Conserv
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                                                                                                                                                                                                           PubMed=9628581;
wa K., Miyajima
                                                                                                                                                                                                                                                                                                                           Primates;
                                                                                                                                                                                                                                                                                                                                             Chordata;
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Pred. No.
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NON_TER 1 1 1 0 SEQUENCE 768 AA: 82680 MW; B97A932B44883536 CRC64; 0uery Match 2.9%; Score 8; DB 4; Length 768; Best Local Similarity 100.0%; Pred. No. 36; Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0; 14 AALLLIGL 21
Gaps

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/cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/BCTUS_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
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   US-08-195-967-2
US-09-472-940-2
US-08-466-545-10
US-08-66-545-10
US-08-66-5982-44
US-08-468-560C-8
US-08-476-862-8
US-08-477-347-17
US-08-478-45A-51
US-08-974-186-51
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US-08-98-195-4478-11
US-08-98-15-4478-11
US-08-98-15-4478-11
US-08-98-15-4478-11
US-08-98-15-6498-15
US-08-995-139-15
US-08-995-139-15
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US-09-112-6498-15
US-09-112-6498-15
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US-08-195-967-2
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Patent No.
Query Match
Best Local Similarity
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ALIGNMENTS

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; TYPE: amino a
; TOPOLOGY: lir
; MOLECULE TYPE:
US-08-147-784-2
                                                                                                                                                                                                                                            COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, V
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/147,784
FILING DATE: 03-NOV-1993
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Smith, Willaim M
REGISTRATION NUMBER: 05,223
REFERENCE/DOCKET NUMBER: 05490A-22
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 336-2400
                                                                                                                                                               TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 277 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Godfrey, Wayne
APPLICANT: Buck, David
APPLICANT: Engleman, Edgar G.
TITLE OF INVENTION: RECEPTOR ON THE SURFACE OF ACTIVATED
TITLE OF INVENTION: CD4+ T-CELLS: ACT-4
NUMBER OF SEQUENCES: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US
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No. 5821337
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100.0%;
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Score 277; DB 2;
Pred. No. 1.4e-260;
                     Length 277;
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                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/195, FILING DATE: 10-FEB-1994 CLASSIFICATION: 424 ATTORNEY/AGENT INFORMATION: NAME: Smith, William M REGISTRATION NUMBER: 30,223 REFERENCE/DOCKET NUMBER: 05490 TELECOMMUNICATION INFORMATION: TELEPHONE: (415) 326-2400
                                                                                                                                                                                         TELEPHONE: (415) 326-24
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PATENT: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/195,967
                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: 379 LYLL
CITY: Palo Alto
STATE: California
COUNTRY: US
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TITLE OF INVENTION: LIGAND (ACT-4-L) TO
TITLE OF INVENTION: CD4+ T-CELLS
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 277 amino acids
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                                                                                                                                       TYPE: amin
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RRDQRLPPDAHKPPGGGSFRTPIQEEQADAHSTLAKI 277
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Patent No. 6
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CITY: RC
STATE: N
COUNTRY:
ZIP: 208
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; TOPOLOGY: 1; MOLECULE TYPE: US-09-006-353A-12
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                                                                                                                                                                                                                                                                                                                                              TELEFAX: (301) 309-85: INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/09/
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: BROCKES, ANDERS A
REGISTRATION NUMBER: 36,37
REFERENCE/DOCKET NUMBER: F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: WEI, YING-FEI
APPLICANT: YU, GUO-LIANG
APPLICANT: GENTZ, REINER
APPLICANT: RUBEN, STEVEN
APPLICANT: RUBEN, STEVEN
TITLE OF INVENTION: TUMOR NECROSIS FACTOR RECEPTOR
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: (301) 309-8504
                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 277 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      241 RRDQRLPPDAHKPPGGGSFRTPIQEEQADAHSTLAKI 277
                                                                                                                                                                                                                                                                        STRANDEDNESS:
                                                                PGVDCAPCPPGHFSPGDNQACKPWINCTLAGKHTLQPASNSSDAICEDRDPPATQPQETQ 180
NTVCRPCGPGFYNDVVSSKPCKPCTWCNLRSGSERKQLCTATQDTVCRCRAGTQPLDSYK 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GPPARPITVQPTEAWPRTSQGPSTRPVEVPGGRAVAAILGLGLVLGLLGPLAILLALYLL 240
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Pred. No. 1.4e-260;
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                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 530
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/147,
FILING DATE: 03-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: Smith, Willaim M
REGISTRATION NUMBER: 30,223
REGISTRATION NUMBER: 0549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (415) 326-24 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Engleman, Edgar G.
TITLE OF INVENTION: RECEPTOR ON THE SURFACE OF
TITLE OF INVENTION: CD4+ T-CELLS: ACT-4
                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION: TELEPHONE: (415) 326-2400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
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                  121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0, Version
                                                 61
                                                                             61
                                                                                                                                                                                          Local
                                                                                                                                                                                                                                                                                   TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                  LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/OFILING DATE: 06-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE:
                                                                                                                           1 MCVGARRLGRGPCAALLLLGLGLSTVTGLHCVGDTYPSNDRCCHECRPGNGMVSRCSRSQ
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No. 6277962
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                                                            NTVCRPCGPGFYNDVVSSKPCKPCTWCNLRSGSERKQLCTATQDTVCRCRAGTQPLDSYK 120
                                                                                                           MCVGARRLGRGPCAALLLLGLGLSTVTGLHCVGDTYPSNDRCCHECRPGNGMVSRCSRSQ
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              PGVDCAPCPPGHFSPGDNQACKPWTNCTLAGKHTLQPASNSSDAICEDRDPPATQPQETQ
                                               NTVCRPCGPGFYNDVVSSKPCKPCTWCNLRSGSERKQLCTATQDTVCRCRAGTQPLDSYK
1 Similarity
277; Conserv
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SYSTEM: PC-DOS/MS-DOS
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Pred. No. 1.4e-260;
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RESULT 6
US-08-050-319B-44
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Patent No.
                                                                                                              Matches
                                                                                                                             Best
                                                                                                                                       Query Match
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                                                                                                                                                                                                                                                                TELEX: 66141 PENNIE INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                     ID NO:
ACTERISTICS:
56 amino acids
STRANDEDNESS: S1'
TOPOLOGY: 1'
OLECULE "'
166'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Greene, Mark I.
APPLICANT: Murali, Ramachand
APPLICANT: Takasaki, Wataru
                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION: NAME: Coruzzi, Laura A
                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/0 FILING DATE: 30-MAY-1997 CLASSIFICATION: 530 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY:
STATE:
                                                     NAME: Coruzzi, Laura A
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 00
                                                                                                                                                                                                                                                                                                            TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE
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                                                                                                                          Local
                                                                                                                                                                                                                                                                                                              TELEPHONE: 650-493-4935
TELEFAX: 650-493-5556
                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER:
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56; Conserv
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100.0%; Pr
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ANALOGUES DESIGNED FROM BINDING SITES
NECROSIS FACTOR RECEPTOR SUPERPAMILY A
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0; Mismatches
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hes 0;
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Sequence

Application US/08050319B

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ATTORNEY/ACEPAT
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                                                                                                                                                                                                                                                                                                                                                            Sequence 44, Application US/08465982 Patent No. 5863786
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                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: ROBbins, Roberta L.
REGISTRATION NUMBER: 33,208
REFERENCE/DOCKET NUMBER: 5150
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 617-8999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (415) 327-3231
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                       STREET: STREET: CITY: Palo Alto CITY: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: 11
MOLECULE TYPE:
                                                                                                                                                                                                                                                 APPLICANT: M.Feldmann, P.W. Gray,
APPLICANT: M.J.C. Turner, F.M Brennan
TITLE OF INVENTION: Modified human TNFalpha (Tumor
TITLE OF INVENTION: Necrosis Factor alpha) Receptor
NUMBER OF SEQUENCES: 57
                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: Reed & Robbins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: M.Feldmann, P.W. Gray,
APPLICANT: M.J.C. Turner, F.M. Brennan
TITLE OF INVENTION: Modified human TNFalpha (Tumor
TITLE OF INVENTION: Necrosis Factor alpha) Recepto
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      138 NQACKPWTNCTL 149
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CITY: Palo Alto
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 41 amino acids
TYPE: amino acid
STRANDEDNESS: single
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APPLICATION NUMBER:
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US/08/465,982
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GENERAL INFORMATION:
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Best Local Similarity
Matches 12; Conserv
                                                                                                                                                                                                                                                                                                      ZIP: 22040-0747
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                APPLICATION NUMBER: US/08/46
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
CTASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MURPHY JR., GERLAD M.
REGISTRATION NUMBER: 28,977
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (415) 327-3231
INFORMATION FOR SEQ ID NO:
                                                                                                          INFORMATION FOR SEQ ID NO:
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REGISTON NUMBER: 33,208
REFERENCE/DOKET NUMBER: 51:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 617-8999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: DNA CODING FOR HUMAN CELL SURFACE TITLE OF INVENTION: ANTIGEN NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
                                                                    SEQUENCE CHARACTERISTICS
LENGTH: 133 amino acid
                                                                                                                                           TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-205-8000
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APPLICANT: ITOH, Naoto
APPLICANT: YONEHARA, Shin
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ATTORNEY/AGENT INFORMATION:
NAME: Robbins, Roberta L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER:
 MOLECULE TYPE:
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TYPE: amino acid
STRANDEDNESS: single
                                 STRANDEDNESS:
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                                                                                                                              TELEFAX:
                                                                                                                                                                                 REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: FALLS CHURCH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: BIRCH, ST
STREET: P.O. BOX 747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY:
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                                                                    133 amino acids
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protein
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7 100.0%; Pr/
7 0;
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Pred. No.
                                                                                                                                                                                   20-4393P
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RESULT 10
US-08-477-347-17
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                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Watches 12; Conserv?
                                                                                                                                                                                                                                                                                                                                     ; MOLECULE TYPE: protein US-08-219-237B-8
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US-08-219-237B-8
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                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/219,237B
FILING DATE: 28-MAR-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/872,129
FILING DATE: 22-APR-1992
CLASSIFICATION: 435
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: James M. Hellwege
REGISTRATION NUMBER: 28,808
REFERENCE/DOCKET NUMBER: 516762
INFORMATION FOR SEQ ID NO: 8:
                                                                                                     Sequence 17, Application US/08477347 Patent No. 6232446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 8, Appra-
Sequence 8, Appra-
No. 5874546
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                        GENERAL INFORMATION:
                                                        APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 139 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: YONEHARA, Shin
TITLE OF INVENTION: DNA Coding for Human Cell Surface Antigen
NUMBER OF SEQUENCES: 11
                            APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            138 NQACKPWINCTL 149
                                                                                                                                                                                                                           138 NQACKPWINCTL 149
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                                                                                                                                                                                                 110 NOACKPWINCTL 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: James W. Hellwege
STREET: P.O. Box 2266 Eads Station
CITY: Arlington
STATE: Virginia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
              OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Application US/08219237B
                                                                                                                                                                                                                                                                                                                                                                                                  139 amino acids
                                                                                                                                                                                                                                                4.3%; Score 12; illarity 100.0%; Pred. No. Conservative 0: Micro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ITOH, Naoto
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                            METT,
                                        BELETSKY, Igor
                                                        WALLACH, David
BIGDA, Jacek
                                                                                                                                                                                                                                                                                                                                                                       linear
Igor
NN: TNF LIGANDS
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RESULT 11
US-08-476-862-8
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STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-477-347-17
                                                                                                                                                                                                                                                                                                Sequence 8, Application US/08476862 Patent No. 6262239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: IL 106

FILING DATE: 08-JUL-1993

ATTORNEY/AGENT INFORMATION:

NAME: TOWNSEND, G. KEVIN

REGISTRATION NUMBER: 34,03
                                                                                                                                                                                                   APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: WALLACH-10
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 248633
                                                                     STREET: 419 CONTROL WAShington STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
PRIOR APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatil
OPERATING SYSTEM: PC-DOS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 140 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
                                                                                                                                                                                     APPLICANT: ENGELMANN, Hartmut
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 248633
                                                                                                                                                                     NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                         138 NQACKPWINCTL 149
                                                                                                                                                                                                                                                                                                                                                                                            111 NOACKPWINCTL 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W.
                                                             ZIP: 20004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              140 amino acids
                                                                                                                          419 Seventh Street, N.W.
                                                                                                                                                                                                                                                                    WALLACH,
                                                                                                                                                                                                                       METT, Igor
                                                                                                                                                                                                                                  BELETSKY, Igor
                                                                                                                                                                                                                                                     BIGDA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        USA
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, Jacek
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Pred. No.
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PC-DOS/MS-DOS

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RESULT 12
US-08-974-022-51
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Best Local Similarity 100.0%;
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 51,
Patent No. 6
                                                                                                                                                                                                                                                                                                APPLICANT: Boyle, Willaim J.
APPLICANT: Lacey, David L.
APPLICANT: Calzone, Frank J.
APPLICANT: Chang, Ming-Shi
TITLE OF INVENTION: OSTEOPROTEGERIN
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: BROWDY, ROGER L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: WAI
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 90339
FILLING DATE: 18-MAY-1989
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 06-APR-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 91229
FILING DATE: 06-AUG-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
IL 107267
              PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                              ADDRESSEE: Amgen Inc.
STREET: 1840 Dehavilland Drive
CITY: Thousand Oaks
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
                                   CLASSIFICATION:
                                                  APPLICATION NUMBER: US/0 FILING DATE: 12-DEC-1995
                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                 STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY:
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APPLICATION NUMBER: 08/577,788
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Application US/08974022
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                                                                                                                                                                                                                USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
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Pred. No.
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Best Local S
Matches 12
                                                        Matches
                                                                     Query Match
Best Local 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Boyle, Willaim J.
APPLICANT: Lacey, David L.
APPLICANT: Calzone, Frank J.
APPLICANT: Chang, Ming-Shi
TITLE OF INVENTION: OSTEOPROTEGERIN
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: Winter, Robert B.
REFERENCE/DOCKET NUMBER:
INFORMATION FOR SEQ ID NO: 51
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO:
                                                                                                                                          STRANDEDNESS: single TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: li
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135 NQACKPWTNCTL 146
                138 NQACKPWTNCTL 149
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Amgen Inc.
STREET: 1840 Dehavilland Drive
CITY: Thousand Oaks
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
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STRANDEDNESS: sir
                                                                                                                                                                                         TYPE: amino acid
                                                                                                                                                                                                       LENGTH:
                                                                                                                                                                                                                                                                                             FILING DATE:
                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 91320-1789
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                                                                      Similarity
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                                                                                                                                                                                                     205 amino acids
                                                       ilarity 100.0%;
Conservative
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100.0%; Pred. No.
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                                                                      Score 12; pred. No.
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                                                        Mismatches
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RESULT 15
US-08-974-186-51
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US-08-795-447A-51
                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: BOYL, I
APPLICANT: Lacey, I
APPLICANT: Calzone
APPLICANT: Chang, I
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 51,
                                                                                                                                                                                                                                                                                                                      Patent No.
                                                                                                                                                                                                                                                                                                                                    Sequence 51,
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Best Local Similarity 100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Winter, Robert B.
REFERENCE/DOCKET NUMBER:
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Calzone, Frank J.
APPLICANT: Chang, Ming-Shi
TITLE OF INVENTION: Osteoprol
NUMBER OF SEQUENCES: 53
                                                                                                                                                                                APPLICANT: Chang, Ming-Shi
TITLE OF INVENTION: OSTEOPROTEGERIN
NUMBER OF SEQUENCE: 53
CORRESPONDENCE ADDRESS:
             COMPUTER REALIABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 205 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Amgen Inc.
STREET: One Amgen Center Drive
CITY: Thousand Oaks
STATE: California
                                                                                                                                ADDRESSEE: Amgen Inc.
STREET: 1840 Dehavilland Drive
CITY: Thousand Oaks
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                 COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12;
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linear
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Lacey, David L.
Calzone, Frank J.
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Lacey, David L.
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PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                 Willaim J.
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; Pred. No.
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; TOPOLOGY: 1:
; MOLECULE TYPE:
US-08-795-446B-51
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US-08-795-446B-51
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Winter, Robert B.
REFERENCE/DOCKET NUMBER: A-3
INFORMATION FOR SEQ ID NO: 51:
SEQUENCE CHARACTERISTICS:
LENGTH: 205 amino
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 51, Appli
Patent No. 6288032
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Best Local Similarity 100.0%;
                                                                                           REFERENCE/DOCKET NUMBER: A INFORMATION FOR SEQ ID NO: 51: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                         CLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                          SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Boyle, Willaim APPLICANT: Lacey, David L. APPLICANT: Calzone, Frank APPLICANT: Chang, Ming-Shi
                                                                                                                                              ATTORNEY/AGENT INFORMATION: NAME: Winter, Robert B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: OSTEOPROTEGERIN NUMBER OF SEQUENCES: 53
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                                             STRANDEDNESS
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                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Thousand Oaks
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                                                                TYPE:
                                                                                                                                                                                            APPLICATION NUMBER:
                                                                                                                                                                                                                                                            APPLICATION NUMBER:
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                                                                             CENGTH:
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amino acid
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1840 Dehavilland Drive
                                                                               205
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Lacey, David L.
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linear
                            bs: single
linear
                                                                             amino acids
             protein
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Pred. No.
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0.00058;
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Pred. No.

Immunex Corporation

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; TOPOLOGY: linear; ; MOLECULE TYPE: protein; SEQUENCE DESCRIPTION: SEQ ID NO: 7: US-08-097-827-7
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US-08-494-574-7
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; Sequence 7, Application US/08097827
; GENERAL INFORMATION:
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Best Local Similarity
Matches 12; Conserv
                                                                                                                                                                           Sequence 7, Application US/08494574 Patent No. 5783665
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                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: 206-587-0730
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 206 amino acids
TYPE: amino acid
    APPLICANT: Baum, Peter
APPLICANT: Goodwin, Ray
APPLICANT: Fanslow, William
APPLICANT: Gayle, Richard
TITLE OF INVENTION: No. 5783665el Cytokine Which is a Ligand for
TITLE OF INVENTION: OX40
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION UMBER: US/08/097,827
FILING DATE: 23-Jul-1993
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia A.
REGISTRATION NUMBER: 34,693
REGISTRATION NUMBER: 34,693
                                                                                                                                                                                                                                                                                                 136 NOACKPWINCTL 147
                                                                                                                                                                                                                                                                                                                                      138 NQACKPWTNCTL 149
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ADDRESSEE: Immunex Corporation
STREET: 51 University Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 2806 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: Novel Cytokine Which is a Ligand for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Baum, Peter
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ZIP: 98101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                             Conservative
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Fanslow, William
Gayle, Richard
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100.0%; Pred. No. 0.00058
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hes 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 11, Application US/08097827
GENERAL INFORMATION:
APPLICANT: Baum, Peter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
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Best Local Similarity
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APPLICATION NUMBER: US/08/494,574

FILING DATE: 22-JUN-1995

CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/097,827

FILING DATE: 23-JUL-1993

ATTORNEY/AGENT INFORMATION:

NAME: PERKINS, PATTICIA A.

REGISTRATION NUMBER: 34,693

REGISTRATION NUMBER: 34,693

REGISTRATION NUMBER: 3806

TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: 206-587-0730
INFORMATION FOR SEQ ID NO: 7
SEQUENCE CHARACTERISTICS:
LENGTH: 206 amino acids
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STREET: 51 Uni
CITY: Seattle
STATE: WA
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
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                                                                            CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/097,827
FILING DATE: 23-Jul-1993
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                          COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                          ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 13
                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: Novel Cytokine Which is a Ligand for $\sf OX40$
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                                                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
NAME: Perkins, Patricia A. REGISTRATION NUMBER: 34,693 REFERENCE/DOCKET NUMBER: 2806
                                                                                                                                                                                                                                                                                                         STATE: WA
                                                                                                                                                                                                                                                                                                                         STREET: 51 Un:
CITY: Seattle
                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Immunex Corporation
STREET: 51 University Street
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Fanslow, William
Gayle, Richard
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100.0%; Pred. No.
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; MOLECULE TYPE: Protein ; SEQUENCE DESCRIPTION: SEQ ID NO: 11: US-08-097-827-11
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                                                                                                                            ; MOLECULE TYPE: protein US-08-494-574-11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
Matches 12; Conserv
                                                 Matches
                                                               Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/097,827
FILING DATE: 23-JUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia A.
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2806
                                                                                                                                                                                                                          TELEPHONE: 206-587-0730 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Baum, Peter
APPLICANT: Goodwin, Ray
APPLICANT: Fanslow, William
APPLICANT: Gayle, Richard
TITLE OF INVENTION: No. 5783665el Cytokine Which is
TITLE OF INVENTION: OX40
                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Rel
CURRENT APPLICATION DATA:
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CORRESPONDENCE ADDRESS:
138 NQACKPWINCTL 149
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OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/494,574 FILING DATE: 22-JUN-1995 CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                            TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
                                                                                                                                                                                        LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                        amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WA
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                                                                                                                                                                                        438 amino acids
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51 University Street
                                                 Conservative
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                                           100.0%; Pi
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100.0%; Pred. No.
                                                               4.3%; Score 12;
00.0%; Pred. No.
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                                         , DB 1; L. do. 0.0012; 0;
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RESULT 22
US-08-995-659-15
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                                                                                                          Sequence 15, Application US/08995659 Patent No. 6242213
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Best Local
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APPLICANT: Galibert, Laurent
APPLICANT: Maraskovsky, Eugene
TITLE OF INVENTION: Receptor Activator of NF-kappaB
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: USSN 08/772,330
FILING DATE: 23 DECEMBER 1996
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2851-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: USSN 08/813,509
FILING DATE: 07 MARCH 1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/772,330
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APPLICATION NUMBER: USSN 60/064,671
FILING DATE: 14 OCTOBER 1997
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MEDIUM TYPE: Floppy disk
                 APPLICANT: Anderson, Dirk M. APPLICANT: Galibert, Laurent APPLICANT: Maraskovsky Eugene TITLE OF INVENTION: Ligand for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION: TELEPHONE: (206)587-0430
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OPERATING SYSTEM: Apple Operatin
SOFTWARE: Microsoft Word for Po
                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 625 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/996,139 FILING DATE: 22 DECEMBER 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE:
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9; Conserv
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51 University Street
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                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                      Ligand for Receptor Activator of NF-kappaB : 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Apple Operating System 7.5. ft Word for Power Macintosh
                                                                                                                                                                                                                                                                                         %; Score 9; DB 3
%; Pred. No. 1.3
0; Mismatches
                                                                                                                                                                                                                                                                                                            DB 3;
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RESULT 23
US-09-215-649A-15
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                                                                                                                                                                                                                                                           Sequence 15, Application US/09215649A
Patent No. 6271349
GENERAL INFORMATION:
GBILDERT, Laurent
Maraskovsky, Eugene
TITLE OF INVENTION: Receptor Activator of NF-kappaB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (206)233-0644
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RECISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2852-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 22 DECEMBER 1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 60/064,671
FILING DATE: 14 OCTOBER 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,693
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/772,330
FILING DATE: 23 DECEMBER 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/813,509
FILING DATE: 07 MARCH 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5\5
SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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ADDRESSEE: Immunex Co
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Match 3.2%; Score 9; DB 4; Local Similarity 100.0%; Pred. No. 1.3; es 9; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Seattle
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                  ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
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                                                                                                                                 CITY: Seattle
STATE: WA
                                                                                                                                                                        ADDRESSEE: Immunex Corporation, Law Department STREET: 51 University Street
                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ΨA
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                                                                                                                                                                                                                                           OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     USA
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                                                                                                            USA
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US-09-105-390-20
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FILING DALL.

CLASSIFICATION:

CLASSIFICATION DATA:

CLASSIFICATION UNBER: 60/050,675

APPLICATION NUMBER: 60/050,675

FILING DATE: 25-JUN-97

ATTORNEY/AGENT INFORMATION:

NAME: Petithory, Joanne R.

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 20, Application US/09105390 Patent No. 6288303 GENERAL INFORMATION:
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NAME: PETITIOLY, 295
REGISTRATION NUMBER: P42,995
REFERENCE/DOCKET NUMBER: 200
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 50-324-0880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (206)233-0644 INFORMATION FOR SEQ ID NO: 15:
                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/105,390
FILING DATE: Filed herewith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Rodriguez, Raymond TITLE OF INVENTION: Rice Beta TITLE OF INVENTION: and Genes NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       170 CKPWTNCTL 178
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APPLICATION NUMBER: USSN 08/813,509
FILING DATE: 07 MARCH 1997
APPLICATION NUMBER: USSN 08/72,330
FILING DATE: 23 DECEMBER 1996
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,693
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CITY: Palo Alto
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity hes 9; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Dehlinger & Associates STREET: 350 Cambridge Ave., Suite
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 625 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 2851-A TELECOMMUNICATION INFORMATION: TELEPHONE: (206)587-0430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/215,649A
FILING DATE: 17-Dec-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear MOLECULE TYPE: proteir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: <Unknown> PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM: Apple Operating System 7.5. SOFTWARE: Microsoft Word for Power Macintosh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: 08/996,139
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DB 4;

Length 625; Indels

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Gaps

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RESULT 26
US-09-124-671-19
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Best Local Similarity
"hes 7; Conserva
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-124-671-17
: Sequence 17, Application US/09124671A
: Patent No. 6160088
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; FRAGMENT TYPE:
US-09-105-390-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: ROCLMANA, James
APPLICANT: Mayhew, Mark
APPLICANT: Hoe, Mee
TITLE OF INVENTION: KDEL RECEPTOR INHIBITORS
FILE REFERENCE: 31488
                                                                                                                               GENERAL INFORMATION:
APPLICANT: ROCHMAN, James
APPLICANT: Mayhew, Mark
APPLICANT: HOe, Mee
TITLE OF INVENTION: KDEL RECEPTOR INHIBITORS
FILE REFERENCE: 31488
                                                                                                                                                                                                                      Sequence 19, Application US/09124671A Patent No. 6160088
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/124,671A
CURRENT FILING DATE: 1998-07-29
NUMBER OF SEQ ID NOS: 42
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 17
LENGTH: 105
TYPE: PRT
ORGANISM: Artificial Sequence
                             CURRENT APPLICATION NUMBER: US/09/124,671A CURRENT FILING DATE: 1998-07-29 NUMBER OF SEQ ID NOS: 42 SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 19 LENGTH: 119 TYPE: PRT
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               ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13 AALLLLG 19
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TELEX:
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b; Pred. No. 6.9
0; Mismatches
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Pred. No.
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RESULT 27
US-09-124-671-21
; Sequence 21, Applica
; Patent No. 6160088
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CURRENT FILING DATE: 1998-07-29
NUMBER OF SEQ ID NOS: 42
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 21
LENGTH: 109
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; OTHER INFORMATION: chimeric mouse TSP3-KDEL US-09-124-671-19
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US-09-124-671-13
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Best Local Similarity
' has 7; Conserv
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                                                                           ; OTHER INFORMATION: chimeric rat comp US-09-124-671-13
                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/124,671A
CURRENT FILING DATE: 1998-07-29
NUMBER OF SEO ID NOS: 42
SOFTWARE: FASTSEQ for Windows Version 3.0
SEO ID NO 13
LENGTH: 115
TYPE: PRT
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APPLICANT: ROTHMAN, James
APPLICANT: Mayhew, Mark
APPLICANT: Hoe, Mee
TITLE OF INVENTION: KDEL RECEPTOR INHIBITORS
FILE REFERENCE: 31488
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Best Local S
   Matches
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                Query Match
Best Local
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APPLICANT: Mayhew, Mark
APPLICANT: Hoe, Mee
TITLE OF INVENTION: KDEL RECEPTOR INHIBITORS
FILE REFERENCE: 31488
                                                                                                          ORGANISM: Artificial Sequence FEATURE:
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 Similarity 100 7; Conservative
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2.5%; Score 7; DB (100.0%; Pred. No. 24)
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100.0%; Pred. No.
Live 0; Mismatc
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   0;
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APPLICANT: Rothman, James
APPLICANT: Mayhew, Mark
APPLICANT: Mayhew, Mark
APPLICANT: Hoe, Mee
TITLE OF INVENTION: KDEL RECEPTOR INHIBITORS
FILE REFERENCE: 31488
CURRENT APPLICATION NUMBER: US/09/124,671A
CURRENT FILING DATE: 1998-07-29
NUMBER OF SEQ ID NOS: 42
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 15
LENGTH: 115
TYPE: PRT
TYPE: PRT
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US-08-478-039-110
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US-09-124-671-15
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Best Local S
Matches 7
             COMPUTER READABLE FOORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTION DATA:
APPLICATION UMBER: US/08/478,039
FILING DATE: 07-JUN-1995
CLASSIFICATION DATA:
APPLICATION UMBER: US 08/379,072
FILING DATE: 25-JAN-1995
PRIOR APPLICATION UMBER: US 08/379,072
APPLICATION UMBER: US 08/379,072
APPLICATION UMBER: US 07/912,292
FILING DATE: 10-JUL-1995
PRIOR APPLICATION DATA:
APPLICATION UMBER: US 07/912,292
PRIOR APPLICATION DATA:
APPLICATION UMBER: US 07/856,281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 110, Application US/08478039 Patent No. 5681722
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Newman, Roland A.
APPLICANT: Hanna, Nabil
APPLICANT: Raab, Ronald W.
TITLE OF INVENTION: Recombinant Antibodies for Human Therapy
NUMBER OF SEQUENCES: 114
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: USA
ZIP: 22313-1404
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CITY: Alexandria
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100.0%; Pred. No. 24;
cive 0; Mismatches
US 07/735,064
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                                                                    Query Match 2.5%;
Best Local Similarity 100.0%;
Matches 7; Conservative (
                                                                                                                                                                                                                               TELEPHONE: 703-836-6620
TELEFAX: 703-836-2021
INFORMATION FOR SEQ ID NO: 110:
SEQUENCE CHARACTERISTICS:
LENGTH: 128 amino acids
                                                                                                                                                                                                                                                                                                                      REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-160
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 25-JUL-1991
ATTORNEY/AGENT INFORMATION:
NAME: Teskin Esg., Rohin
15 ALLLLGL 21
|||||||
4 ALLLLGL 10
                                                                                                                                                                                                                                                                                                                                                         NAME: Teskin Esq., Robin L. REGISTRATION NUMBER: 35,030
                                                                                                                                                                                               TYPE: amino acid TOPOLOGY: linear
                                                                      Score 7; DB 1;
Pred. No. 26;
0; Mismatches
                                                                                                        Length 128;
                                                                          Indels
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Search completed: June 18, 2002, 14:28:49 Job time: 207 sec

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Title:
Perfect score:
Sequence:
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No.
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Maximum DB
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6:
7:
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277
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| SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1981 DAT: *
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Copyright (c) 1993 - 2000 Compugen Ltd.
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AAR79904
AAB3532909
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AAR76996
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ABG28518	ABG01306	ABG25452	AAM40633	AAB53079	AAB80233	AAU12327	AAM38847	AAY95342	AAB24398	AAY97290	AAY13365	AAY32926	ABG28519	AAM95526	ABG18405	AAW75070	ABG01305	AAW87708	ABG01184	ABG18404	ABG01304	AAY44302	AAE01994	AAE04427	AAE08739			8	9	832	95	28	AAR81882	98	AAR81881	9	AAB98752	88	
1 human	l human	Novel human diagno	Human polypeptide			PRO224	polyper	PRO224 anti	PRO224 prot	assoc	no acid sec	Вm		n reprod	dia	n secret	l human diagn	н	l human	l human	human diagn	acrosome re	RANK (rece	receptor a	receptor a	e receptor	nding prote	NF-kB rece	NF-kB rec	ne osteoclas	bind	O/Fc	mid pDC406/ox	e OX40 ext	se type-II mem	protein. Un	y	Human secondary si	

ALIGNMENTS

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AC AAR7
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AAR74737;

AAR74737 standard;

Protein;

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21-NOV-1995 (first entry)

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			Domain		Modified-site		Modified-site		Cleavage-site		Cleavage-site		Peptide	Key		Homo sapiens.		Cell surface re		ACT-4 cell surf
		<pre>/note= "transmembrane domain"</pre>	214240	/note= "glycosylation site"	160162	/note= "glycosylation site"	146148	/note= "signal cleavage site"	2425	/note= "signal cleavage site"	2223	/note= "signal peptide"	124	Location/Qualifiers				Cell surface receptor; ACT-4; T-lymphocyte; T-cell; immune system.		ACT-4 cell surface receptor protein.

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RESULT
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ID ARAT
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                                        Homo
                                                                                                   grait versus host disease; immune response; transplantation; autoimmune disease; inflammation; HIV; human immunodeficiency virus; HTLV; human T lymphocyte virus; inflammatory house virus;
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Pred. No. 2.7e-250;
; Mismatches 0;
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RESULT

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18-AUG-1999;
20-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention provides the protein and coding sequences of the human tumour necrosis factor receptors TRI3 and TRI4. These sequences are useful in the diagnosis and treatment of many diseases, including cancer, autoimmune diseases, cardiovascular disorders, allergies, neurodegenerative diseases, graft rejection, inflammation, aneurysms and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nucleic acids encoding 2 human tumor necrosis factor receptor polypeptides ((TRI3) and (TRI4)), useful for the prevention, diagnosis and treatment of, e.g. cancers, acquired immune deficiency syndrome and hypohidrotic ectodermal dysplasia.
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                      RRDQRLPPDAHKPPGGGSFRTPIQEEQADAHSTLAKI
                                                                                                              GPPARPITVQPTEAWPRTSQGPSTRPVEVPGGRAVAAILGLGLVLGLLGPLAILLALYLL 240
                                                                                                                                                                                 pgvdcapcppghfspgdnqackpwtnctlagkhtlqpasnssdaicedrdppatqpqetq
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
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RESULT
                                cc activities, and can be used in gene therapy. The TRID polynucleotides are useful for detecting complementary polynucleotides. TRID proteins and complementary polynucleotides. TRID proteins and complementary polynucleotides. TRID proteins and complement of tumours, resistance to polynucleotides are useful in the treatment of tumours, resistance to comparative bacteria and viruses, restenosis and graft versus host disease. They are also useful for inducing proliferation of T-cells, endothelial colls and certain haematopoietic cells, to regulate antiviral responses and to prevent certain autoimmune diseases after stimulation of TRID by can agonist or TRAIL binding facilitator. The antibodies which bind TRID casceive associated with increased or decreased apoptotic cell death. The TRID collynucleotides, proteins, antibodies, agonists and antagonists are useful in the diagnosis, treatment or prevention of: (a) cancer; (b) autoimmune disorders; (c) diseases associated with increased concers apoptosis; (d) cardiovascular disorders; and (e) viral infection. The present sequence represents a tumour necrosis factor receptor used in comparison with TRID in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                    The present invention describes the human TRID protein (tumour necrosis factor (TNF) related apoptosis inducing ligand (TRAIL) receptor without intracellular domain, also referred to as tumour necrosis factor receptor 5 (TNFR-5 or TR5)). TRID has cytostatic, immunosuppressive, nootropic, neuroprotective, antiviral, antiinflammatory, anticonvulsant, antiparasitic, cardiant, anti-HIV, antiparkinsonian and vasotropic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          immunosuppressive; neuroprotective; antiviral; antiinflammatory; anticonvulsant; antiparasittc; cardiant; anti-HTV; antiparkinsonian; gene therapy; restenosis; graft versus host disease; tumour; cancer; apoptotic cell death related disease; autoimmune disorder; cardiovascular disorder; viral infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nucleic acid encoding a TRID polypeptide, also referred to as necrosis factor receptor 5, useful in the diagnosis, treatment prevention of cancer, autoimmune disorders and viral infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Fig 2; 285pp; English.
  Sequence
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RESULT
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the OX-40 antigen was identified (expressed on the surface of activated autoantigen specific CD4+ T-cells present at the site of inflammation but absent on CD4+ T-cells at non-inflammatory sites) and cDNA encoding the antigen was isolated. PCR primers were designed and used to clone murine OX-40 CDNA by PCR from RNA isolated from murine CD4+ T-cells activated with concanavalin A. Then the murine OX-40 CDNA was used to probe a cDNA lambda gtll library from human activated T lymphocytes to obtain human OX-40 CDNA. The published patent application states that the OX-40 CDNA sequence is also in SQ ID no. 1, but this sequence is not present in the spec. A nucleic acid having the sequence in SQ ID no 1 and
                                                                                                                                                                                                                                                                                 Antigen OX-40 is specifically expressed on the cell surface of antigen activated T-cells. A specially, for example, CD4+ T-cells. A human cDNA encoding the human OX-40 homologue was cloned as follows. Using the Experimental Autoimmune Encephalomyelitis model in rats
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nucleic acid encoding an activated T-cell antigen, Ox-40 - used develop prods. for detection and therapy of conditions mediated activated T-cells, eq. multiple sclerosis, rheumatoid arthritis,
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                                                                                                                                                                                                                                                                                                                                                                                                             Fig 11; 91pp;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   etc.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local S
Matches 114
                                                                         The present invention describes peptides and peptide analogues which correspond in primary sequence to a binding loop of a tumour necrosis factor receptor (TNF-R) superfamily member. The compounds are especially designed from a binding loop of TNF-R p55. They are capable of inhibiting TNF binding to its cellular receptors and may be used to inhibit the biological activities of TNF-They may be used in treating TNF-associated conditions such as scute and chronic inflammatory responses, septic shock, cachexia, autoimmunity, graft-versus-host disease, skin allergic reactions, immune complex disease, g. oral, transplantation rejection and malaria. Administration is, e.g. oral,
                                                                                                                                                                                                                                                                                                                        WPI;
                                                                                                                                                                                                                                                                 New compounds designed from a binding loop of a tumour necrosis factor receptor - are capable of inhibiting the biological activities of tumour necrosis factor, e.g., in treating inflamm
                                                                                                                                                                                                                                                                                                                                                 Greene MI, Murali R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tumour necrosis factor receptor; TNF-R; autoimmune diseases; inflammation; septic shock; cachexia; graft versus host disease; skin allergic reaction; immune complex disease; malaria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the
                                      transdermal, transmucosal, pulmonary, subcutaneous, intravenous intramuscular. Parenteral dosage is 0.1-5 mg/kg/day. The present sequence represents an extracellular Cys-rich domain of TNF-R fr
                                                                                                                                                                                                                             Disclosure;
                                                                                                                                                                                                                                                         or autoimmune diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                         03-DEC-1998
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                                     sequence represents
                                                                                                                                                                                                                                                                                                                                                                            (UYPE-) UNIV
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                                                                                                                                                                                                                                                                                                                                                                                                                             29-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     transplantation rejection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TNF-R extracellular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29-APR-1999
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                        invention
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                                                                                                                                                                                                                            Fig 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                      97US-0866545
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                                                                                                                                                                                                                            78pp;
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100.0%;
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Pred. No. 3
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RESULT
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Best Local :
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                                   and immunocoulatory activities, and are tumour necrosis factor (TNF)-related activation-induced cytokine (TRANES)/ receptor activator of NF-kappaB ligand (RANK) inhibitors. The method is useful for treating diseases characterised by bone loss such as osteoporosis, Paget's disease, metastatic bone disease, rheumatoid arthritis or periodontal disease, and modulating dendritic cell maturation. T cell proliferation, and/or CD40 receptor systems. The present sequence represents an extracellular Cys-rich domain of a tumour necrosis factor receptor (TNF-R) superfamily member, which is used in the exemplification of
                                                                                                                                                                                                            The
                                                                                                                                                                                                                                                                                                                                                                                               (MYPE-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   osteoclastogenesis; bone loss; bone resorption; osteopathic; cytost antirheumatic; antiarthritic; antiinflammatory; immunomodulatory; tumour necrosis factor-related activation-induced cytokine; TRANCE; receptor activator of NF-kappaB ligand; RANK; osteoporosis;
                                                                                                                                                               osteoclastogenesis and bone resorption. Osteoclastogenesis and bone resorption inhibiting peptide analogues from the present invention have osteopathic, cytostatic, antirheumatic, antiarthritic, antiinflammatory
Sequence
                                                                                                                                                                                                                                        Disclosure;
                                                                                                                                                                                                                                                                                                              WPI;
                                                                                                                                                                                                                                                                                                                                       Aoki K
                                                                                                                                                                                                                                                                                                                                                                                                                                      28-JUL-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Paget's disease; metastatic bone disease; rheumatoid arthr periodontal disease; modulating dendritic cell maturation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tumour necrosis factor receptor; TNF-R; inhibition; osteoclast;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human TNF-R extracellular Cys-rich domain OX40 SEQ ID NO:10
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                                                                                                                                                                                                                                                                                                                                                                 (BARO/)
                                                                                                                                                                                                                                                                                                                                                                                (HORN/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          64
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                                                                                                                                                                                                            present invention describes a method for inhibiting
                                                                                                                                                                                                                                                                 of peptides and inhibiting ostec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CRPCGPGFYNDVVSSKPCKPCTWCNLRSGSERKQLCTATQDTVCRCRAGTQPLDSY 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sapiens
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                                                                                                                                                                                                                                                                                                             2001-182866/18
                                                                                                                                                                                                                                                                                                                                                          JNIV
AOKI K.
JORNE W C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                         UNIV PENNSYLVANIA
                                                                                                                                                                                                                                                                                                                                    Horne WC,
58
                                                                                                                                                                                                                                       Fig
                        invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2000WO-US20510
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Ä
                                                                                                                                                                                                                                                               \mbox{\it a} and peptide analogs which are \mbox{\it TRANCE/RANK} inhibitors, osteoclastogenesis and bone resorption -
                                                                                                                                                                                                                                                                                                                                                                                                                                      99US-0146090
                                                                                                                                                                                                                                       ۲;
                                                                                                                                                                                                                                     81pp; English.
                                                                                                                                                                                                                                                                                                                                       Baron
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CD40 receptor system.
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                                                                                                                                                                                                                                                                                                                                      Murali
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               osteopathic; cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          arthritis;
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Query Match Best Local Similarity

15.2%;

Score 42; Pred. No.

1.7e-31; DB 22;

Length 58;

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241 RRDQRLPPDAHKPPGGGSFRTPIQEEQADAHSTLAKI

Query Match Best Local S Matches 37

37; Conservative

13.4%; 5c. 100.0%; Pr

Score 37; DB Pred. No. 5.3

DB 22; 5.3e-27

Length 37;

Indels

0,

Gaps

0

.3e-27;

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AAB84272
ID AAB8
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RESULT
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                                                                                                                      The present sequence represents a secondary signalling sequence, which is linked to a non-natural stimulatory primary signalling motif to produce a cytoplasmic signalling motif. The primary motif is efficient at mediating immune cell signal transduction, particularly when incorporated in an intracellular signalling domain of a chimeric receptor. The primary signalling motif can be combined in any way so as to achieve the desired level of activation (or inhibition) of a number of secondary messenger cascades. The signalling motifs are useful in therapy and in the manufacture of medicament for treating or preventing disease in humans or animals. They are are useful for treating inmunocleficions within infectious diseases e.g. human immunocleficions within the main form infectious diseases e.g. human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    chimeric receptor; inflammatory disease; autoimmune disease; ast eczema; congenital disease; cystic fibrosis; sickle cell anemia; dermatological disease; psoriasis; neurological disease; multiple sclerosis; transplant-related disease; metabolic diseas crean transplant rejection; graft versus host disease;
                                                                                                                                                                                                                                                                                                                                                                                                                            WPI;
                                                                                                                                                                                                                                                                                                                            Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Secondary signalling sequence used to make cytoplasmic signalling motif.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAB84272
                                                             sickle cell anemia, dermatological diseases e.g. psoriasis, neurological diseases e.g. multiple sclerosis, transplant-related disease e.g. organ
                                                                            immunodeficiency virus (HIV) infections, inflammatory/autoimmune diseases such as asthma and eczema, congenital diseases e.g. cystic fibrosis, sickle cell anemia, dermatological diseases e.g. psoriasis, neurological
                                                                                                                                                                                                                                                                                                                                                                                            Novel
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Finney
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1999;
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Sequence
                                             transplant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         idiopathic disease; diabetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (CELL-) CELLTECH CHIROSCIENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                            2001-389718/41
                                                                                                                                                                                                                                                                                                                                                          cytoplasmic signalling protein and chimeric receptor pr
l for treating HIV infection, asthma, eczema, psoriasis,
osis, contain non-natural stimulatory primary signalling
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MH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      standard;
                                            rejection, graft versus
37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     primary signalling
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                                                                                                                                                                                                                                                                                                                          45pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     peptide;
                                cancer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cancer.
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                                               host
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                                               disease,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cell;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          metabolic disease;
                                                 metabolic/idiopathic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         signal transduction;
                                                                                                                                                                                                                                                                                                                                                                                         protein,
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AAB98799
                                                                                                                      The invention relates to a novel nucleic acid encoding an adaptor CC receptor protein comprising an extracellular ligand-binding domain, a CC transmembrane domain and an intracellular signalling domain. The CC intracellular signalling domain comprises the cytoplasmic portion of at CC least one adaptor protein, and the extracellular ligand-binding domain CC is not CDB or a major histocompatibility complex (MHC) class I protein. CC The adaptor receptor protein and the nucleic acid encoding it are useful in therapy. They are useful in the manufacture of a medicament for the CC treatment or prevention of disease in humans and animals. They are useful in the treatment of infectious diseases (e.g. HIV infection). CC congenital diseases (e.g. cystic fibrosis and sickle cell anaemia). CC dermatological diseases (e.g. cystic fibrosis and sickle cell anaemia). CC dermatological diseases (e.g. cystic fibrosis and sickle cell anaemia). CC multiple sclerosis), organ transplant rejection, graft-versus-host cell disease and metabolic/idiopathic diseases such as diabetes and cancer. CC invention. Secondary signalling motif used in the CC invention. Secondary signalling motif used in the CC invention. Secondary signalling motif used as used as components of the adaptor receptor protein of the invention. Motifs were isolated from CD28, CD134 and CD154.
Query Match
Best Local S
Matches 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     antisickling; antipsoriatic; neuroprotective; immunosuppressive; antidiabettc; cytostatic; HIV infection; inflammation; autoimmune disease; cystic fibrosis; sickle cell anaemia; psoriasis; neurological disease; organ transplant rejection; diabetes; cancer; graft-versus-host disease; adaptor receptor protein; CD28; CD134; CD154; primary signalling mottif; secondary signalling mottif.
                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 26; Page 35; 52pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel polynucleotide encoding adaptor receptor protein useful for treating human immunodeficiency virus (HIV) infection, asthma, cystic fibrosis, multiple sclerosis, organ transplant rejection, diabetes and cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-328790/34.
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37; Conserv
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                                                                                            37
 Conservative
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                 13.4%;
100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             motif SB34a.
Score 37; DB; Pred. No. 5.3
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                 DB 22;
5.3e-27;
                                  Length 37;
 Indels
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Gaps
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Matches

h 13.4%; Similarity 100.0% 37; Conservative

.08;

Score 37; Pred. No.

.8e-27;

Length 41; Indels

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Gaps

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Mismatches

241 RRDQRLPPDAHKPPGGGSFRTPIQEEQADAHSTLAKI 277

rrdqrlppdahkppgggsfrtp1qeeqadahstlaki 39

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AAB84292
ID AAB8
XX AAB8
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                                                               transduction, particularly when incorporated in an intracellular signalling domain of a chimeric receptor. The primary signalling motif can be combined in any way so as to achieve the desired level of activation (or inhibition) of a number of secondary messenger cascades. The signalling motifs are useful in therapy and in the manufacture of medicament for treating or preventing disease in humans or animals. They are are useful for treating human patients suffering from infectious diseases e.g. human immunodeficiency virus (HIV) infections, inflammatory/autoimmune diseases such as asthma and eczema, congenital diseases e.g. cystic fibrosis, sickle cell anemata, dermatological diseases e.g. soriasis, neurological diseases e.g. multiple sclerosis, transplant-related disease e.g. organ transplant rejection, graft versus host disease, metabolic/idiopathic disease e.g. diabetes, and cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Stimulatory primary signalling motif; immune cell; signal transduction; chimeric receptor; inflammatory disease; autoimmune disease; asthma; eczema; congenital disease; cystic fibrosis; sickle cell anemia; dermatological disease; psoriasis; neurological disease; multiple sclerosis; transplant-related disease; metabolic disease; organ transplant rejection; graft versus host disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present sequence represents a secondary signalling sequence, which may be linked to a non-natural stimulatory primary signalling motif The primary motif is efficient at mediating immune cell signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel cytoplasmic signalling protein and chimeric receptor protein, useful for treating HIV infection, asthma, eczema, psoriasis, multiple sclerosis, contain non-natural stimulatory primary signalling motif -
       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 2; Fig 4; 45pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1999;
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       41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       disease;
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                                                                                                                                                          CC The invention relates to novel primary signalling motifs containing CC a consensus amino acid sequence. These motifs are extremely CC efficient at mediating immune cell signal transduction, particularly CC when incorporated into an intracellular signalling domain of a chimeric CC receptor. Nucleic acids that encode, and polypeptides that contain, CC these primary signalling motifs are useful in medicine and research. CC They are useful in therapy, or in the manufacture of a medicament for CC treating or preventing disease in humans or in animals. These diseases include infections (e.g. HIV (human immunodeficiency virus) infection), CC inflammatory or autoimmune diseases (e.g. asthma or eczema), congenital CC diseases (e.g. cystic fibrosis or sickle cell anaemia), dermatological CC diseases (e.g. psoriasis), neurological diseases (e.g. multiple CC sclerosis), organ transplant rejection or graft-versus host disease, or CC present sequence is one of a large number of primary and secondary CC signalling motifs used in the invention. Primary signalling motifs are Sequences that transduce either a stimulatory or an inhibitory signal, CC which regulates primary activation of the T cell receptor (TCR) complex. Secondary motifs impart secondary or co-stimulatory signalling capacity CC to a molecule in T cells. GS linkers have been incorporated at each CC end of the present sequence to facilitate cloning.
                                       Query Match
Best Local
Matches 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; primary signalling motif; sequence block; SB; immunosuppressive; secondary signalling sequence; antimicrobial; antiinflammatory; secondary signalling sequence; continuous anti-HTV; antiasthmatic; dermatological; neuroprotective; cytostatic; anti-HTV; antiasthmatic; antisickling; antipsoriatic; antidiabetic; gene therapy; diabetes; immune cell signal transduction; infection; inflammation; cancer; autoimmune disease; congenital disease; psoriasis; neurological disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New nucleic acids encoding polypeptides with expanded primary signaling motifs, for use in gene therapy, particularly for treating or preventing infections, inflammations or autoimmune diseases in humans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1999;
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                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example
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241 RRDQRLPPDAHKPPGGGSFRTPIQEEQADAHSTLAKI
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                                                        Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fig
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                                         Conservative
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                                                        13.4%;
100.0%;
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                                                      Score 37;
Pred. No
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                                         Mismatches
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                                                                        Length
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RESULT JAAB988222
ID AAAB988222
ID AAAB988222
ID AAAB988222
ID AAAB988222
ID AAB988222
ID AAB98822
ID AAB9882
ID AAB9882
ID AAB98822
ID AAB9882
ID AAB9888
ID AAB988
                                                                                    The invention relates to a novel nucleic acid encoding an adaptor creceptor protein comprising an extracellular ligand-binding domain, a C transmembrane domain and an intracellular signalling domain. The cintracellular signalling domain comprises the cytoplasmic portion of at least one adaptor protein, and the extracellular ligand-binding domain. The cintracellular signalling domain comprises the cytoplasmic portion of at least one adaptor protein, and the extracellular ligand-binding domain. The cintracellular ligand-binding domain comparises the cytoplasmic portion of at least one adaptor receptor protein and the nucleic acid encoding it are useful complex (MHC) class I protein. The treatment of infections diseases (e.g. HIV infection), complex compenity of infections diseases (e.g. HIV infection), complex congenital diseases (e.g. cystic fibrosis and sickle cell anaemia), compenital diseases (e.g. cystic fibrosis and sickle cell anaemia), compenital diseases (e.g. psoriasis), neurological diseases (e.g.) compenital diseases (e.g.) compenity and secondary signalling motifs (compenity and secondary signalling motifs (compenity activation of the T cell receptor (TCR) complex. Secondary compenits and compenity be compenity of the adaptor receptor protein of the used as components of the adaptor receptor protein of the view of the contains a GS linker at the N-terminus to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             antisickling; antipsoriatic; neuroprotective; immunosuppre
antidiabetic; cytostatic; HIV infection; inflammation;
autoimmune disease; cystic fibrosis; sickle cell anaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel polynucleotide encoding adaptor receptor protein useful for treating human immunodeficiency virus (HIV) infection, asthma, cy; fibrosis, multiple sclerosis, organ transplant rejection, diabete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAB98822 standard; Peptide; 41
   Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2001-328790/34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Finney HM,
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                                                                         tacilitate
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fig
       41
                                                                      cloning
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99GB-0025854
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  52pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SB34.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               thma, cystic
diabetes and
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5.8e-27;

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RESULT 1
AAB98752
ID AAB9
                  when incorporated into an intracellular signalling domain of a chimeric creeptor. Nucleic acids that encode, and polypeptides that contain, these primary signalling motifs are useful in medicine and research. They are useful in therapy, or in the manufacture of a medicament for treating or preventing disease in humans or in animals. These diseases include infections (e.g. HIV (human immunodeficiency virus) infection), inflammatory or autoimmune diseases (e.g. asthma or eczema), congenital diseases (e.g. cystic fibrosis or sickle cell anaemia), dermatological diseases (e.g. psoriasis), neurological diseases (e.g. multiple sclerosis), organ transplant rejection or graft-versus-host disease, or metabolic/idiopathic diseases (e.g. diabetes or cancer). The present sequence is a secondary signalling sequence used in the co-stimulatory signalling capacity to a molecule in T cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Loc
Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                    efficient at mediating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New nucleic acids encoding polypeptides with expanded primary signaling motifs, for use in gene therapy, particularly for treating or preventing infections, inflammations or autoimmune diseases in humans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     organ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (CELL-) CELLTECH CHIROSCIENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10-MAY-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; primary signalling motif; CD28; immunosuppressive; secondary signalling
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human secondary signalling
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 241
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16;
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signalling
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Page
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lawson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             relates to novel primary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      43pp; English.
sequences
                                                                                                                                                                                                                                                                                                                                                                                                   immune cell signal transduction, particularly an intracellular signalling domain of a chime
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sequence.
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isolated
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from human CD28, CD134
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          motifs containing
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Query Match,

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Length 32;

Query Match Best Local Similarity

4.3%; 100.0%;

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DB 22; 0.0048;

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RESULT 1
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                                                                                                                                                                                                                                                                                                                   The present invention relates to a method for treating conditions leading to bone loss. The method comprises administering a purified and isolated osteoprotegerin (OPG) protein (AMF57836-AMF57838 and AMB66974-AMB66976) in conjunction with other substances such as tumour necrosis factor-alpha (TNF-alpha) inhibitors, interleukin (IL)-6, -8 and -18 inhibitors, ICE modulators, fibroblast growth factor (FGF)1-10 modulators and/or platelet activating factor (PAF) antagonists. The method is useful for treating conditions leading to bone loss such as rheumatoid arthritis, multiple sclerosis, osteoprosis, osteomyelitis and asthma. The method is also useful for treating inflammation, systemic lupus erythematosus (SLE) and graft-versus-host disease (GVHD). Other diseases that can be treated include acute pancreatitis, Alzhelmer's disease, anorexia, atherescales are constant conditions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0x40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Treating conditions leading to bone loss sucmultiple sclerosis and asthma, comprises and osteoprotegerin protein in conjunction with interleukin and tumor necrosis factor alpha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bone loss; osteoprotegerin; OPG; rheumatoid arthritis; hyperalgesia; multiple sclerosis; osteoprotesis; osteomyelitis; asthma; inflammation; systemic lupus crythematosus; graft-versus-host disease; septic shock; acute pancreatitis; Alzheimer's disease; anorexia; atherosclerosis; pacoronary condition; myocardial infarction; cancer; diabetes; psoriasis endometriosis; fever; glomerulonephritis; inflammatory bowel disease;
                                                                                                                                                                        include acute pancreatitis, Alzheimer's disease, anorexia, atherosclerosis, coronary conditions (e.g. myocardial infarction), cancer, diabetes, endometriosis, fever, glomerulonephritis, hypera inflammatory bowel disease, ischaemia, pain, Parkinson's disease, partial transported that the partial transported the partial transported the partial transported that the partial transported the partial transported that the partial transported transpo
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Sequence
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09-DEC-1999;
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                                                                                                                                          inflammatory bowel disease, psoriasis and septic shock.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (AMGE-) AMGEN INC.
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99US-0457647
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thes 0;
                                                                                                                                               sequence
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Matches 12
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                                OX40; cytokine;
OX40/Fc.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           \tt OX40; OX40-L; cytokine; cell surface molecule; membrane <code>glycoprotein</code> .
                                                                                                                                                                                                                                                                                                                                                                                                                                                 glycoprotein cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               This sequence encodes the extracellular domain of OX40, a membrane glycoprotein present on the CD4 positive subset of activated T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New isolated DNA encoding the OX40 ligand polypeptide - also ve and host cells, used to produce recombinant ligand used in e.g. prim. T cell culture, to modulate immune response etc.
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 Mus sp
                                                                                  Mouse OX40 extracellular domain.
                                                                                                                  25-SEP-1998
                                                                                                                                                   AAW48977;
                                                                                                                                                                              AAW48977 standard; Protein; 206 AA.
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DB; AAT00826.
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12; Conservative
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                                              cell antigen; TH-2 immune response; OX40-L;
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Pred. No.
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0.0048;
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present sequence represents the mouse OX40 extracellular domain The extracellular domain of OX40 is its ligand binding domain. The cDNA (AAV32640) encoding OX40 extracellular domain was used in the construction of the chimeric OX40/Fc cDNA (AAV32640). The invention claims for a murine OX40-L cytokine (AAW48975) that binds to the OX40 murine T cell antigen. The OX40-L protein is claimed to be useful for co-stimulation of T-cell production and in binding assays for detecting OX40 or its homologues. The OX40-L protein is also claimed
WPI; 1995-357992/46.
N-PSDB; AAT00829.
                                                                                                                                                                                                                                                                             OX40; OX40-L; cytokine; cell surface molecule; pDC406/OX40/Fc*; membrane glycoprotein.
                                                                                                                                                                                                                                                                                                                               Plasmid pDC406/OX40/Fc*
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22-JUN-1995;
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nes 12; Conserv
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DB; AAV32640.
                                                                                IMMUNEX
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                                                Fanslow WC,
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. 0.0048;
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     WPI; 1998-427099/36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Key
Region
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22-JUN-1995;
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m. T cell culture,
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mutant"
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mutant"
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                                                       Gayle
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RESULT 1
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Best Local S
Matches 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present sequence represents the OX40/Fc fusion protein that contains the extracellular domain of mouse OX40 fused to the mutated Fc region of the human IgG1 antibody. The fusion protein was used for detecting cDNA clones encoding an OX40 ligand. The invention claims for a murine OX40-L cytokine (AAW48975) that binds to the murine T cell antigen, OX40. The OX40-L protein is claimed to be useful for co-stimulation of T-cell production and in binding assays for detecting OX40 or its homologues. The OX40-L protein is also claimed to generate a TH-2 immune response.
                                                                  binding protein (OBM-BP) of preventive and/or treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OBM-BP; OBM binding protein; osteoclast formation bone metabolic disease; osteoporosis; therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31-MAR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Purified polypeptide OX-40 ligands - for co:stimulation of T-cell production and binding assays for OX-40 and homologues
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Sequence
                                   osteoporosis.
be used as bi
                                                                                                                                   Claim 1; Page 17-18; 18pp; Japanese.
                                                                                                                                                                        A new
                                                                                                                                                                                                         N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                            07-DEC-1999
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                                                                                                  This sequence is the
                                                                                                                                                                                                                                                     (SNOW ) SNOW BRAND MILK PROD CO (SANY ) SANKYO CO LTD.
                                                                                                                                                                                                                                                                                                         24-MAR-1998;
                                                                                                                                                                                                                                                                                                                                           20-OCT-1998;
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DB; AAZ49022.
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                                                                                                                                                                      protein, a DNA and its application
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12; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 438
                                   biochemical
   201
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                                                    Substances
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sequence
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                                                 osteoclast formation promoting factor (OBM)
-BP) of the invention. The protein is useful as a
aating agent for bone metabolic diseases such as
ices which inhibit the binding of OBM to OBM-BP can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26pp; English.
                                 reagents
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0.0091;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          promoting
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3.2%;

Score Pred.

9; DB No. 3;

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201;

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RESULT :
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                                                    The present sequence represents murine osteoclast differentiation CC and activation receptor (ODAR). The present invention describes CC osteoprotegerin (OPG) binding protein. Host cells transfected with CC vectors containing nucleic acid molecules encoding OPG binding protein CC are used to produce recombinant OPG binding protein. OPG binding protein is used in binding assays to determine osteoprotegrin (OG) in biological CC samples; to screen for specific binding agents (particularly agonists and antagonists, including intracellular proteins); to raise Ab (useful CC in immunoassays for detection of OPG binding protein to ODAR. The CC compounds that modulate binding of OPG binding protein to ODAR. The CC opg binding protein encoding Sequences, e.g. screening for related CC OPG binding protein encoding sequences, e.g. screening for related CC opg binding protein models, while complementary capuances are used for antisense regulation of OPG binding protein complementary complementary soluble forms of OPG binding protein, particularly soluble CC diseases, e.g. osteoporosis, bone loss caused by arthritis or of operation of the protein of operation of the particularly soluble contents of OPG binding protein, particularly soluble of operations, paget's disease, periodontal disease, with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
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16-APR-1997;
23-JUN-1997;
Sequence
                          osteoporosis, looser agents that promote
                                                                                                                                                                                                                                                                                                                                                                 Example 12;
                                                                                                                                                                                                                                                                                                                                                                                                             Nucleic acid encoding osteoprotegrin binding protein - useful for, e.g. treating bone diseases by modulating osteoclast differentiation
                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Boyle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (AMGE-) AMGEN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               osteoporosis; osteoclast maturation; bone disease; metastasis; ODAR hypercalcaemia; osteoclast differentiation and activation receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Osteoprotegerin binding
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                                                                                                                                                                                                                                                                                                                                                                                                for diagnosis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                disease.
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625
                                                                                                                                                                                                                                                                                                                                                               Fig 10; 47pp;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             in binding protein; OPG osteoclast maturation;
                             loosening of prostheses,
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97US-0842842.
97US-0880855.
AA,
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                                                                                                                                                                                                                                                                                                                                                               English.
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bone disease; metastasis; C
                                            optionally
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                                              combination with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
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Query Match Best Local Similarity

3.2%; 100.0%;

Score 9; 1 Pred. No.

DB 19; . 7.8;

Length 625

Query Match
Best Local Similarity
Matches 9; Conserv

Conservative

0;

Mismatches

Indels

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Gaps

0;

3.2%; 100.0%;

Score 9; | Pred. No.

). DB 7. 19;

Length 625

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AAW69958
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                                                                     CC factor-kappab (NF-kB)) polypetide which is a homolog of the human RANK. CC RANK is a member of the tumour necrosis factor (TNF) family. A soluble can may be used for inhibiting activation of NF-kB, by contacting a cell cexpressing membrane-associated RANK with a soluble RANK which binds to CC RANK ligand (RANKL). RANKL polypeptides can activate RANK and can be cused to induce maturation of dendritic cells and enhance their collusted rank polypeptide composition may also be used for regulating an collumnume or inflammatory response. Inhibition of NF-kB by RANK antagonists compose that result from triggering of RANK, e.g. in treating toxic concepts that result from triggering of RANK, e.g. in treating toxic concepts of sused to identify inhibitors of RANK. RANKL polypeptides can also be used in adjunct therapy for disease concepts used to identify inhibitors of RANK. RANKL polypeptides can inflammatory response, and also for protecting RANK. RANKL polypeptides con inflammatory response, and also for protecting RANK. RANKL polypeptides con inflammatory response, and also be used in diplunct therapy for disease con also be used to identify inhibitors of RANK. RANKL polypeptides con inflammatory response, and also for protecting RANK. RANKL polypeptides con inflammatory response, and also for protecting RANK. Rayresing cells con firalpha. The products can also be used for detection and drug
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23-DEC-1996;
07-MAR-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 14; Pages 62-64; 80pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New isolated ligand for receptor activator of NF-kappa B - used to develop products for augmenting an immune response for inhibiting a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1998-377657/32.
N-PSDB; AAV41379.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RANK; necrosis factor-kappa B; NF-kB; immune response; inflammatory response
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   08-OCT-1998
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Sequence
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   625
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96US-0059978.
97US-0813509.
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Best Local S
Matches 9
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23-DEC-1996;
07-MAR-1997;
                                                                                                                                                                                  This represents the murine muRANK (receptor activator of necrosis factor kappaB (NF-kB)) polypetide which is a homolog of the human RANK. Is a member of the tumour necrosis factor (TNF) family. Host cells transformed or transfected with an expression vector comprising the RANK encoding nucleic acid can be used to produce recombinant RANK protein. The soluble RANK may be used for inhibiting activation of NF-kB, by contacting a cell expressing membrane-associated RANK with a soluble RANK which binds to RANK ligand (RANK). The soluble RANK polypeptide composition may also be used for regulating an immune or inflammatory response. Inhibition of NF-kB by RANK antagonists may be useful in ameliorating negative effects of an inflammatory response that result from triggering of RANK, e.g. in treating toxic shock or sepsis, graftversus-host reactions, or acute inflammatory reactions. They can also be used in adjunct therapy for disease characterised by nepplastic cells
                                                                                                                                                                                                                                                                                                                                                                                                         Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RANK; necrosis factor-kappa B; NF-kB; receptor activator; human; immune response; inflammatory response; toxic shock; sepsis; RANKL; RANK ligand; tumour necrosis factor; TNF; murine.
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                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                              New isolated receptor activator of necrosis factor-kappa B for, e.g. developing products for regulating an immune or inflammatory response, treating toxic shock or sepsis
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170 ckpwtnctl 178
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ckpwtnctl 178
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DB; AAV41373.
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                                                         Similarity
9; Conser
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                                                         Conservative
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96US-0059978.
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                                                                   3.2%; Score 9;
100.0%; Pred. No.
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                                                                                                                                                                        products can also be used
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RESULT 2
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Best Local Similarity
Matches 9; Conser
                                                                                   Mouse; receptor; RANK; Receptor activator of NF-kappaB; osteoclast activity; immune response; inflammatory response; excess bone resorption; osteoclast generation; bone loss; osteoporosis; Paget's disease; bone cancer; cancer; hypercalcemia; osteoclastogenesis;
                                                                                                                                                                                                                                                                                                                                                                                                                            This sequence is the osteoclast formation promoting factor (OBM) binding protein (OBM-BP) of the invention. The protein is useful as a preventive and/or treating agent for bone metabolic diseases such as osteoporosis. Substances which inhibit the binding of OBM to OBM-BP can be used as biochemical reagents.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OBM-BP; OBM binding protein; osteoclast formation bone metabolic disease; osteoporosis; therapy.
                                                                          Paget's disease; bone cancer; cancer; hypercalcemia; osteoclastogenesi metastasising cancer; osteoclast differentiation; signal transduction.
                                                                                                                                                    A mouse receptor activator of NF-kappaB designated RANK
                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 10; Page 15-16; 18pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A new protein, a DNA and its application
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         regulating osteoclast generation and inhibiting osteoclast generation in individuals inflicted with excess bone resorption. Especially, the RANK protein is used to treat individuals at risk for excess bone loss, osteoporosis, Paget's disease, bone cancer and cancers associated with hypercalcenia. The RANK protein ameliorates the effects of excess bone loss, by binding to its ligand and inhibiting binding of other cells expressing RANK. It thus decreases osteoclastogenesis when administered into metastasising cancer, such as breast cancer, multiple myeloma, melanomas, lung cancer, prostrate, hematologic, head and neck, and renal which metastasise to bone and induce bone breakdown by locally disrupting normal bone remodelling, by disrupting the osteoclast differentiation pathway. This results in the reduction in the number of osteoclasts, lesser bone resorption and relief from the negative effects of hypercalcenia. The RANK protein also ameliorates systemic effects by interfering with I/II signal transduction that leads to the differentiation of osteoclast precursors into osteoclasts.
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Best Local
                                                                                                                                               Murine; receptor activator of nuclear factor kappaB; RANK; NF; tumour necrosis factor; TNF; TNF receptor associated factor; TRAF; immune response; inflammatory response; graft-versus-host reaction; toxic shock; sepsis; acute inflammatory reaction; bone resorption; anti-apoptotic signal; therapy; immunosuppressant; anti-inflammatory
                                                                                       Mus
Peptide
                                                                                                                                                                                                                                                                                                                                        Murine receptor activator of NF kappaB (RANK) protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAE08739 standard; Protein;
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excess bone resorption, and for inhibiting osteoclast activity,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (Receptor activator of NF-kappaB). The protein is used to regulate osteoclast activity. The RANK protein or its fragments are useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The
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| 170 ckpwtnctl 178
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9; Conserv
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98US-0110836.
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Location/Qualifiers
1..30
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ss effects of osteoporosis, Paget's disease,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     625
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Pred. No.
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                                                                                                                                                     immunosuppressant; anti-inflammatory
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7.
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Score 9; I Pred. No. Mismatches DB 5. 7. . 8; 0

Length 625; Indels

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Sequence

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The patent discloses novel receptor activator of nuclear factor (NF)-

CR kappab (RANK) proteins and their corresponding DNAs. RANK is a member

CR of the tumour necrosis factor (TNF) receptor superfamily and associates

CR with TNF receptor associated factor (TRAF) 2 and 3 which are important

CR in the regulation of immune and inflammatory response. The receptors

CR are useful for regulating immune response and in screening for inhibitors

CR of these receptors. The cytoplasmic domain of RANK is used in developing

CR assays for inhibit interaction of RANK is used in developing

CR assays for inhibit interaction of RANK is used in developing

CR are useful in ameliorating the negative effects of an inflammatory

CR response that result from triggering of RANK, e.g. in treating toxic

CR shock or sepsis, graft versus host reactions, acute inflammatory

CR reactions and the effects of bone resorption. RANK acts as an anti-

CR apoptotic signal and rescue the cells that express RANK from apoptosis.

CR antagonists of RANK-mediated NF-kappa B activation, or to inhibit

CR antagonists of RANK-mediated NF-kappa B activation, or to inhibit

CR are useful for modulating the formation of osteoclastic cells that

CR express RANK. Compounds that interfere with RANK/TRAF6 interactions

CR are useful for modulating the formation of osteoclasts from osteoclast

CR are useful for modulating steeclast function and activities. They

CR are useful in preparing kits for the detection of soluble RANK, or

CR monitor RANK-related activity. The present sequence is RANK proteins

CR of the presence or distribution of RANK transcripts, while the proteins

CR of the presence or distribution of RANK transcripts.

CR of the presence or distribution of RANK transcripts, while the proteins

CR of the presence or distribution of RANK transcripts.
23-DEC-1996;
07-MAR-1997;
14-OCT-1997;
23-DEC-1996;
07-MAR-1997;
22-DEC-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New receptor activator of NF-kappaB (RANK) polypeptides, useful for regulating immune response, in screening for RANK inhibitors, or as adjunct therapy for disease characterized by neoplastic cells that express RANK -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 14; Column 77-80; 47pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Dougall WC,
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                                      from murine.
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DB; AAD15312.
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96US-0772330.
97US-0813509.
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97US-0077181
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31..625
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Best Local s
Matches 9
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07-MAR-1997;
14-OCT-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention relates to receptor activator of NF-chi B (RANK) DNA. RANK is mapped to chromosome 18q22.1 and its ligand (RANKL) to chromosome 13q14. RANK and RANKL are type 1 and type 2 transmembrane. proteins respectively. RANK is a member of the tumour necrosis factor (TNF) superfamily and it closely resembles CD40 in the extracellular region. RANK associates with TNF receptor-associated factor (TRAF) 2 and TRAF3. The DNA molecules are useful for producing ligands of RANK. The ligands are useful for regulating immune response and in screening
  AAE01994,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Key
Region
                                                      AAE01994 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New DNA molecules, useful for producing ligands (which are useful for regulating immune response and in screening for inhibitors of NF-chi receptor activator of NF-chi B (RANK)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        chromosome
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                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 14; Column
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (IMMV ) IMMUNEX CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22-DEC-1997;
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                                                                                                                                                                                                                                  141 CKPWINCTL 149
                                                                                                          27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        inhibitors of RANK.
                                                                                                                                                                                 ckpwtnctl 178
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DB; AAD08716.
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                                                                                                                                                                                                                                                                                         Similarity 100
9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             protein.
                                                                                                                                                                                                                                                                                                                                                                                                                         625
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97US-0077181.
97US-0064671.
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                                                      Protein;
                                                                                                                                                                                                                                                                              3.2%; sur
100.0%; Pr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present sequence is murine RANK
                                                                                                                                                                                                                                                                                      Score 9; DB 2; Pred. No. 7.8
                                                      625
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Mismatches . DB 7 .8; 0;

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Gaps

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3.2%;

Score 9; [

Length 625; Indels

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The present invention relates to a novel receptor, referred to as RANK CC (receptor activator of NF (nuclear factor)-kappaB), a member of TNF CC (tumour necrosis factor) receptor superfamily. RANK is a Type I CC transmembrane protein that interacts with TNF receptor-associated factors (TRAFS). Triggering of RANK by overexpression or co-expression of factors (TRAFS). Triggering of RANK by overexpression or co-expression of factor NF-kappaB, a winguitous transcription factor of the transcription factor NF-kappaB, a winguitous transcription factor that is most extensively utilised in cells of the immune system. CC inhibition of Nf-kappaB by RANK antagonists is useful in ameliorating negative effects of inflammatory reactions, and the effects of excess comparation of pharmaceutical compositions, for infecting target for the preparation of pharmaceutical compositions, for infecting target cells for use in gene therapy applications in diagnosing diseases compared with RANK, and as targets for use in screening assays. They may be used in the treatment or diagnosis of immune system dysfunction. The present invention also encompasses gene therapy methods to correct consecutivating mutations, associated with e.g. familial expansile of correct maino acid sequence is murine RANK (muRANK) protein. This sequence which is a type I transmembrane protein contains a predicted 30 amino acid signal sequence, a 184 amino acid extracellular domain, a 21 amino acid signal sequence, a 184 amino acid extracellular domain, a 21 cmino acid mino acid companies domain and a 390 amino acid cytoplasmic tail.
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Region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mouse; receptor activator of NF-kappaB; RANK; nuclear factor-kappaB; NF-kappaB; tumour necrosis factor; TNF; type I transmembrane protein; TNF receptor-associated factor; TRAF; RANK ligand; RANKL; osteopathic;
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New DNA encoding a receptor activator of NF-kappaB polypeptide for the treatment of Paget's disease and Familial Expansile Osteolysis (FEO) -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Anderson DM, Hughes
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       inflammatory reaction; bone resorption; gene therapy; imm
immune system dysfunction; familial expansile osteolysis;
early onset Paget's disease of bone; EP; cytostatic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2001-329222/34
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625
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Page 80-82;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (receptor activator of NF-kappaB) protein
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197..214
/label- Spacer_region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           English.
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                                                                                                                                                                     Matches
                                                                                                                                                                                                                              The present sequence is a functional mouse acrosome reaction protein, PKDREJ or P3. PKDREJ is a sperm protein involved in binding the sperm to the egg and/or triggering the acrosome reaction. It exhibits homology to human polycystin-1 and surEJ. It can be used to identify antibodies or proteins that block the acrosome reaction and compounds that trigger acrosome reaction in the absence of zona protein can be used to increase fertility and those blocking its action can be used as contraceptives. DNA encoding PKDREJ can be used gene therapy and also as primer or probe for identifying sequences that encode mutant forms of acrosome reaction protein.
                                                                                                                                                                                                                                                                                                                                         Claim 1; Fig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAY44302;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAY44302 standard; Protein;
                                                                      ABG01304;
                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                Harris PC,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       W09964457-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Acrosome reaction protein; P3; Polycystic Kidney Disease and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mouse acrosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29-FEB-2000
        Human; chromosome mapping; gene mapping; gene therapy; forensic;
food supplement; medical imaging; diagnostic; genetic disorder.
                                  Novel human diagnostic protein #1295
                                                      13-FEB-2002
                                                                                        ABG01304 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                            fertility treatment
                                                                                                                                                                                                                                                                                                                                                                    New functional mammalian acrosome reaction protein, useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                 (MEDI-) MEDICAL RES COUNCIL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   10-JUN-1998;
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                                                                                                                                                                      similarity
9; Conserver
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                                                                                                                                                                                                                                                                                                                                                                                                               Hugues JR,
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                                                                                                                                                                      Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       on protein; P3; sperm protein; polycystin-1; suREJ; ey Disease and Receptor for Egg Jelly protein; PKDI fertility; contraceptive; gene therapy; mouse.
                                                    entry)
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Pred. No.
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                                                                                                                                                                      Mismatches
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23-AUG-2000;
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                                                                              ABG18404;
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                                                                                                                                                                                                                                                                                                                                                                                                              polypeptide
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polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics formatics.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic amino acid sequences of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutation responsible for genetic disorders or other traits and to assess biodiversity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Note: The sequence data for this patent did not appear in the specification, but was obtained in electronic format directly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to isolated polynucleotide (I) and
Human; chromosome mapping; gene mapping; gene therapy; forensic;
food supplement; medical imaging; diagnostic; genetic disorder.
                                                                                                                                                                                                                                                                                                ABG18404 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 20; SEQ ID No 31663; 103pp; English
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                                                                                               diagnostic protein
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2000US-0649167
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                                                                                                                                                                                                                                                                           The invention relates to isolated polynucleotide (I) and CD polypeptide (II) sequences. (I) is useful as hybridisation probes. CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome CC and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags CC for identifying expressed genes. (I) is useful in gene therapy techniques (CI). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical consisting of sites expressing (II). (I) and (II) are useful for treating CC disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in CC diagnostics, forensics, gene mapping, identification of mutations CC responsible for genetic disorders or other traits to assess blodiversity and to produce other types of data and products dependent on DNA and CC and to produce other types of data and products dependent on DNA and CC amino acid sequences of the invention.

CC specification, but was obtained in electronic format directly from WIPO or internation in the mino acid sequences of the invention.
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                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                at ftp.wipo.int/pub/published_pct_sequences.
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N-PSDB; AAS82591.
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23-AUG-2000; 2000US-0649167.
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100.0%; Pred. No. 8.1;
mative 0; Mismatches
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